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Result
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                        ၀ ၀
                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                           Score
                                    315
35.88
35.88
35.35
                                                                                                                                                                                                                                                          d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed
is derived by analysis of the total score distribution.
   34.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_032802:*

1: /SIDS1/gcgdata/h
2: /SIDS1/gcgdata/h
3: /SIDS1/gcgdata/h
4: /SIDS1/gcgdata/h
5: /SIDS1/gcgdata/h
6: /SIDS1/gcgdata/h
6: /SIDS1/gcgdata/h
7: /SIDS1/gcgdata/h
8: /SIDS1/gcgdata/h
9: /SIDS1/gcgdata/h
 100.0 315 2

12.1 1664976

11.4 5599 2

11.4 5999 2

11.2 2944528

11.1 2597

11.1 26811

11.0 4084 2

11.0 15122 2
                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                       3: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
4: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
5: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
6: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
6: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
7: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA198.DAT: *
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8: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
9: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
10: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
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14: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
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26: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
27: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
28: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
29: //SIDS1/gcgdata/hold-geneseq/geneseqn-embl/WA199.DAT: *
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
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315
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
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23
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                  AAZ29725
AAV21209
ABL12244
ABL12246
ABA03041
AAI58172
AAX20253
ABL17122
     ABL32774
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            Listeria monocytog
Human polynucleoti
Borrelia burgdorfe
Drosophila melanog
                                                                                 Human lung specifi
Methanococcus jann
Drosophila melanog
Drosophila melanog
                                                                                                                                                                       Description
 immune syste
 AAZ29725
ID AAZ2
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Example 1; Page 35; 40pp; English.
                                A new method for diagnosing, monitoring and staging lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ29725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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Human metastasis a	ABL34604	24	6255	10.3	32.6	
	AAH51761	21	\sim	10.3	32.6	
	ABL18630	23	2351	10.3	32.6	
Human immune syste	ABL33527	24	S	10.4	32.8	
Staphylococcus aur	AAV74349	18	23439	10.5	ω	
Borrelia burgdorfe	AAX20257	20	10749	10.5	33	
Drosophila melanog	ABL21210	23	2319	10.5	ω ω	
1	AAH07311	22	719	10.5	ω ω	
Tumour suppressor	AAS46745	22	38342	10.5	33.2	
Human musculoskele	AAL36479	22	32190	•	33.2	
-	AAS31548	22	5957	10.5	33.2	
genomi	AAS98600	24	140036		33.4	
immune,	AAK85567	22	10616	10.6	33.4	
	AAK85565	22	10616	10.6	33.4	
	ABL33276	24	5675	10.6	33.4	
	ABL32104	24	17869	10.7	33.6	
	AAK68945	22	17700	10.7	33.6	
	AAK68948	22	8344	10.7	33.6	
immune	AAK68947	22	8344	10.7	33.6	
	ABL32087	24	8178	10.7	33.6	
Human immune syste	ABL33159	24	5909	10.7	33.6	
Staphylococcus aur	AAV76716	18	217	10.7	33.6	
Arabidopsis thalia	AAF22303	21	611590	10.7	33.8	
BAC containing rep	AAF22299	21	85680	10.7	33.8	
	ABL33698	24	6084	10.7	33.8	
	AAS61321	24	5647	10.7	33.8	
Human immune syste	ABL33567	24	5647	10.7	33.8	
lococcu	AAV74345	18	3492	•	ω ·	
AKAP10	AAH02339	22	162025	•	34	
Human AKAP10 gene	AAH02340	22	161425	•	34	
odium fa	AAQ13727	12	3088	10.8	w	
immune	ABL33703	24	18624	•		
₽-	ABL33323	24	9741	10.9		
Tumour suppressor	AAS46370	22	6169	10.9		
eotide sequ	919	20	0	11.0	34.8	
Human immune syste	ARI.34155	24	15548	11.0	ب 4.	

ALIGNMENTS

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21-MAY-1998;
                                                                                                                                                    25-NOV-1999
                                                                                                                                                                                   W09960160-A1
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                            Lung Specific Gene; LSG; human; diagnostic marker; prognosticate; lung cancer; diagnosis; ds.
                                                                                                                                                                                                                                                                                        Human lung specific gene-2.
                                                                                                                                                                                                                                                                                                                        27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                  AAZ29725 standard; DNA;
                                                                                                                      12-MAY-1999;
                                                          (DIAD-) DIADEXUS LLC.
2000-116320/10.
                            F, Macina RA,
                                                                                                                                                                                                                                                                                                                      (first entry)
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RESULT
AAAV211209
ID AAV2
XX AAV2
AC AAV2
XX Meth
XX Meth
XX Meth
XX Genc
OS Meth
XX W9enc
OS Meth
XX 2098
XX 2098
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Complete genome sequence of methano-genic archaeon, Methanoccoccus jannaschii - useful in identification of M. jannaschii genome
                                                                                              WPI; 1998-169145/15
                                                                                                                                                   Bult CJ,
                                                                                                                                                                                  (GENO-) INST GENOMIC RES.
(UNII ) UNIV ILLINOIS FOUND.
(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                   22-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09807830-A2
                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coccus jannaschii; methanogenic archaeon; circular chromosome; autotrophic; extrachromosomal element; identification; ds.
                                                                                                                                             Smith HO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jannaschii circular chromosome.
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Pred. No. 8.6e-74;
Mismatches 0;
                                                                                                                                      White OR,
                                                                                                                                        Woese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the complete 1.66-megabase pair genome CC sequence of the Methanococcus jannaschii circular chromosome. The present invention describes M. jannaschii open reading frames from the GC present invention also describes a computer based system CC for identifying fragments of the M. jannaschii genome that are CC means comprising the nucleotide sequences, comprising: (a) data storage by sequence (see AAV21209, AAV21210 and AAV21211), or a nucleotide sequence of the 164976, 58407 or 16550 cc sequence at least 99.9% identical to it; (b) search means for comparing a CC identify a homologous sequence. The method, which is based on whole genome CC in the homologous sequence. The method, which is based on whole genome CC of which consists of 3 physically distinct elements, a large circular CC extra-chromosoma (the 164976 by sequence given in AAV21209), a large circular CC extra-chromosomal element (the 58407 by sequence given in AAV21210), and CC a small circular extra-chromosomal element (the 58407 by sequence given in AAV21210), and CC fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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WPI; 2001-656860/75
                                 Venter JC,
                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                             (PEKE ) PE
                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 31214
                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                        ABL12244 standard; cDNA; 5516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 acaaattttgaaaatagattgtcacacaataaactggagtttatgggaaacatcagtagaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1664976 BP; 568133 A; 264649 C; 258701 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 152-585; 614pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgtatactacatattagctccaaactcagttactggagttgcagcagtagatggtagta 108625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggaaatacaacattccatccctttacagagatcatttacttgcaactcagggataatttgt 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catgtgtattatctacttatgc
                                                              CORP NY
                             Adams M,
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54.28;
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                          PWD,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                            Myers
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5.1;
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RESULT 4
ABL12246/c
ID ABL122
XX
AC ABL122
XX
DT 26-MAR
XX
DT 20-SO;
KW Droso;
KW Dharm;
XX
OS Droso;
YX
PM W0200
XX
PF 23-MA
XX
PF 23-MA
XX
PR 11-JU
XX
PR 11-JU
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PR 11-JU
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PR 11-JU
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PR PF 23-MA
PR PF 23-MA
PR PF PF Went
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PR WPI;
DR P-PS
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PT New
PT gene
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Best Local Similarity
Matches 82; Conser
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 genes from Drosophila
                                                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                         pharmaceutical;
                                                                                                                                                                                                                                                                                                        Drosophila;
                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 31220
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                                                                                                                                                                                                                                                                                                                                                                                                              ABL12246 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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                                                                                                            (PEKE ) PE CORP NY
                                                                                                                                                                               23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5516
              New isolated nucleic
                                          P-PSDB; ABB68143.
                                                                                   Venter
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                                                       2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATTTTTATGTTATTTGTAATAAGATGTTAATACAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caactcaggataatttgtcatgtgtattatctacttatg
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                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                     developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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2000US-0614150
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                                                                                                                                                                                                                                                                                        gene;
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                                                                                                                                                                                                                                                                                                                                                                                                              cDNA; 5999
                                                                                                                                                                                                                                                                                                                                                           entry)
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51.6%;
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                                                                                  PWD,
detection reagent for detecting for elucidating cell signalling
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Pred. No. 5
                                                                                 Myers
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                                                                                                                                                                                                                                                                                                     cell signalling;
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RESULT
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Best Local
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                                                      Chakraborty T, Domann E, Perez-Diaz J, Baquero F, Maduenio E, De Pablos B, Rose M, Voss H;
                                                                    Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Madduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                   vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                           WPI;
                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                  11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                               18-OCT-2001
                                                                                                                                                                                                                                                                                                         WO200177335-A2
                                                                                                                                                                                                                                                                                                                                    Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; gene therapy; vacc. vitamin B12; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes EGD-e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                        (INSP ) INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions
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                            2002-010914/01
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82; Conser
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                                                                                                                                                                                        PASTEUR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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51.6%;
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Genomic sequence for Listeria monocytogenes, useful e.g.

for treatment

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Db 338711 cgatccactccagaaaagctgaggtagaagtactgc 338746
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          14-SEP-2000;
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29-NOV-2000;
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                                             21-JAN-2000;
25-APR-2000;
                                                                                                                                   26-DEC-2000;
                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; ceptripheral nervous system; neuropathy; central nervous system; catheimer's; Parkinson's disease; Huntington's disease; haemosta amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 375.
                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001
                                                                                                                                                                                                                                                 leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAI58172 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the genome sequence of Listeria monocytogenes BGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and proteins (ABB47297-ABB50149) expressed from the present sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and proteins encoded by it are also useful for selecting compounds that monocytogenes and related organisms, and for biosynthesis and proteins encoded by it are also useful for selecting compounds that monocytogenes related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention of Listeria and related bacterial infections, and sted polypeptides \cdot
    ; 2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0653151.
2000US-0693036.
2000US-0727344.
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                                                                                                                              2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                        thrombolytic; drug
                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA; 2597 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 24;
                                                                                                                                                                                                                                               arthritis; inflammation;
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                                                                                                                                                                                                                                                                       haemostatic;
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Best Local S
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       18-JUN-1998;
                                                                             Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                           Borrelia burgdorferi polynucleotide sequence
                                                                  Borrelia burgdorferi
                                                                                                                                                           04-MAY-1999
                                                                                                                                                                                               AAX20253 standard; DNA; 26811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and Alzheimer's, Parkinson's disease, Huntington's diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the ActivinyInhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and cassays discorders.
                                                                                                                                                                                                                                                                                                                                             148 caccttatattcaagtaggtatgactacaaattttgaaaatagattgtcacacaataaac
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                                                                                                                                                                                                                                                                               268 ttt 270
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Wang J,
Zhao QA,
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68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids and polypeptides, useful as central nervous system injuries -
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Wang z,
zhou P,
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
   98WO-US12764.
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Wehrman T,
Goodrich
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Pred. No. 8;
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anac RT;
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Yang Y,
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20-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (BD). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genomic polynucleotide
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                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                                  Drosophila melanogaster
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                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                pharmaceutical;
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                                                                                           23-MAR-2001;
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                                                                                                                                                                                                                                                                             developmental biology;
cal; gene; ds.
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2000US-0614150
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97US-0050359.
97US-0053344.
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49.78;
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13;
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RESULT 9
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ID ABL32774;

XX ABL32774;

XX ABL32774;

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XX DE Human immune system
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XX Human; immune system
XX antiarteriosclerotic
XW antiarteriosclerotic
XW antiinflammatory; antia
XW antiinflammatory; antia
XW acute myeloid leukae
XW acute myeloid leukae
XW gene; ds.
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                                                                                                       antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB0187072).
                                                                                                                                                                   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                            3673
                                                                                                                                                                                                                                                                                                                                                                                                                               3613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4084 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                Human; immune system disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                      263
                                                                                                                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catacatacatacatacatacatatatgtacatacatatgtaaaacttatctcgttgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cttagagatctacagcctccctttaggggacatacaaagtcagttgtgttgcctttgttg
                                                                                                                                                                                                                                                                                                                                                                          gtttttttttgttatcttgtcatga
                                                                                                                                                                                                                                                                                                                                                                                                   gatcatttacttgcaactcaggataa
                                                                                                                                                                                                                                                                                                                                                                                                                               catgttttatttattttctcatttgcaacatcaaatagaacatttgttttgtatttca
                                                                                                                                                                                                                                                                                                                                                                                                                                               taaactggagtttatggaaacatcagtagaaggaaatacaacattccatccctttacaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtcccaccttatattcaagtaggtatgactacaaattttgaaaatagattgtcacacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; SEQ ID NO 2839; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                        immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1059 A; 913 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%;
                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                        associated
                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ŀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.8;
Pred. No. 10;
                                                                                                                                                                                                cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers
                                                                                                                                                                                                                                                                                                                                                                            3698
                                                                                                                                                                                                                                                                                                                                                                                                      288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   872 G; 1240 T;
                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뙆
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                                                                                                                                                                                                                           NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             format directly from
                                                                                                                                                                                                                           747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 or
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RESULT 10
ABL34155/c
ID ABL341
XX ABL341
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XX 26-MAR
AX Human
DE Human
XX Human
XX Human
XX Antiar
KW Antiar
KW Antiar
KW Antirh
KW Antirh
KW Antirh
KW Acute
KW acute
KW neurof
KW gene;
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PN WO2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Д
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                          neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy neurofibromatosis; rheumatoid arthritis; psoriasis; bowel di
                                                                                                                                                                                                                                                                                                                                                                          10376 СТАТААЛААСАТССТАТААЛАЛААТА 10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10496
              W0200200928-A2
                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                               10436
                                                                                                                                                                 antiarteriosclerotic;
                                           Homo sapiens.
                                                                                                                                                                                                              Human immune system
                                                                                                                                                                                                                                              26-MAR-2002
                                                                                                                                                                                                                                                                             ABL34155;
                                                                                                                                                                                                                                                                                                      ABL34155 standard; DNA; 15548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and neular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 747; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 taaacactgactcagattttaagaaataacttttgagaaatagaacaaatgaaatcagtt
                                                                                                                                                                                                                                                                                                                                                                                                 ttgaaaatagattgtcacacaataaa 206
                                                                                                                                                                                                                                                                                                                                                                                                                               TTCATTTACAATTCTTATTTAAAAATACTTACCAAAAATACACTCACTACGAAACAAAATA 10377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              totocaccacttaagtatatotottagagatotacagcotocotttaggggacatacaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9tcagttgtgttgcctttgttgagtcccaccttatattcaagtaggtatgactacaaatt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTCAACAATTAAAACAAAAACTCTTAAAACTATAACTTACGTATATAAAAAATACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACAACCAAACAAAAAAACAAAAACTAAAATATAAAAACCAAAAACTAAAAACTATACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15122 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention provides a number of human immune sare modified by the methylation of cytosines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-EP07537.
                                                                                                                                                                                                         associated gene SEQ ID NO: 2128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3621 A;
                                                                                                                                                          antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.8;
Pred. No. 1:
                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                          nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system associated ytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                              bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15122;
                                                                                                             anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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AAX91990/c
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Best Local S
Matches 66
                                                                                                                                                                                                                                                                                                                                                     14979
                                                     04-NOV-1998;
21-NOV-1997;
                              (GEST ) GENSET
                                                                                         20-NOV-1998;
                                                                                                                03-JUN-1999
                                                                                                                                                          Chlamydia pneumoniae
                                                                                                                                     W09927105-A2
                                                                                                                                                                                  vaccine; neutralising
                                                                                                                                                                                       Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                        Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                        13-SEP-1999
                                                                                                                                                                                                                                                                                AAX91990;
                                                                                                                                                                                                                                                                                                  AAX91990 standard; DNA; 1230025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15548 BP; 4209 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid of for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                          gtttatggaaacatcagtagaaggaaatacaacattccatccctttacagagatcatt 269
                                                                                                                                                                                                                                                                                                                                                                                                               ttatattcaagtaggtatgactacaaattttgaaaatagattgtcacacaaataaactgga 211
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid comprising fragment of chemically modified gene, useful gnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2128; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                  98US-0107078.
97FR-0014673.
                                                                                      06810HI-OM86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%;
55.9%;
                                                                                                                                                                                 epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 C; 2903 G; 8189 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.8; D
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                  ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15548
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Griffais

1999-357842/30

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RESULT 12
AAS46370/c
ID AAS463
XX AAS463
XX AAS463
XX THOMOUR
XX HUMMAN;
KW CANCER
KW CANCER
KW COOS1
XX HOMO S
XX H
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072791 AATTTTCTCCTCAAAAAATTTGTTTATAG 1072762
                                                                                                                                                                                                                                                                                           15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y33879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS46370 standard;
Fragments of chemically modified genes associated with tumour genes and oncogenes, useful in designing primers and probes for
                                                                                              WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 gattgtcacacaataaactggagtttatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 gttgcctttgttgagtcccaccttatattcaagtaggtatgactacaaattttgaaaata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 cttaagtatatctcttagaggatctacagcctccctttaggggacatacaaagtcagttgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTATTTTTAAGTTCTTTAGATAAACAACTTGAGTTCAGGCCAAAACAGTAGAAGA 1072792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   suppressor gene derived chemically modified sequence #92
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                                                                                                                                                                                                        EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation;
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                                                                                                                                                Piepenbrock
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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52.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6169
                                                                                                                                                   Berlin
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249833 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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suppressor

Homo sapiens

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RESULT 13
ABL33323/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oncogenes having a sequence taken from 536 (actually 533 since companies having a sequence taken from 536 (actually 533 since companies 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Ss). The nucleic acid may be a complementary to (Ss). The nucleic acid may be a complementary to (Ss) and sequences complementary to (Ss). The nucleic acid may be a compared to a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an companie of a set of probes associated with CpG dinucleotides e.g. (C cancers and tumours. The probes can also be used in a method for carcers and tumours. The probes can also be used in a method for cascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic parameters, the CC diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the CC diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the CC diseases, by analysing cytosine methylations. The parameters which care disadvantageous to patients. The present sequence is one of the CC are disadvantageous to patients. The present sequence is one of the CC and genes. Sequences with even numbered Seq ID numbers are the CC complementary sequence of the corresponding odd numbered sequence (e.g. ID and ID), ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is missing).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2351
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                                                                          antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analysing diseases associated with cytosine methylation state
                                                                                                                                          neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                 antiarteriosclerotic;
                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                               Human immune
                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                ABL33323;
                                                                                                                                                                                                                                                                                                                                                                        ABL33323 standard; DNA; 9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAATTCCCTTACAAATATATATAAAATAAACTAAAAATATTTTATCTTATATTTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                             system associated gene SEQ ID
                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to a nucleic acid comprising
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                                                                                                                                                                                   antianaemic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                           ВÞ
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Pred. No. 16;
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                                                                                                                                                                                   nootropic;
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RESULT 14
ABL33703/c
ID ABL337
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                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; accute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                        02-JUL-2001; 2001WO-EP07537
                                                                                                                                                              W0200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL33703 standard; DNA; 18624
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and neukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1296; 32pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine methylation
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01-SEP-2000;
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الخاجة
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9741 BP; 2623 A; 195 C; 1863 G; 5060 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system associated gene SEQ ID NO: 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin
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                                                                                                                                                                                                                                                                                    arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.2;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                            psoriasis; bowel disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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RESULT 15
AAQ13727
ID AAQ137
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DT 05-DEC XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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    EP447956-A.
                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum sporozoite antigen N-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ13727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ13727 standard; DNA; 3088 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3411 AAAAATATAATATTCTCCAAAAATTAAATATATCTTTAAAATATAAAAATCCATCTCTAA 3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1676; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 a-tgactacaaattttgaaaaatagattgtcacacaataaactggagtttatggaaacatc 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18624 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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les 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTATACAAATAAAAACTAAAAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-130909/17
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                                                                                                                                                                                                                                                                                                                                                                                                                    gene; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                            /label= sporozoite-antigen
                                                                                                                                                                                                            Location/Qualifiers 948..3086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AG
                                                                              "N-terminal"
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ζ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138;
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abnormal
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Search completed: September 16, 2002, 03:05:06 Job time: 7984 sec
                                                                                                                                                                                           Query Match 10.8%;
Best Local Similarity 61.1%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                           The sequence is useful in the prodn. of polypeptides corresp. in at least one specific epitope with the P. falciparum sporozoite antigen N-terminal. These polypeptides are useful in the prodn. of antimalarial vaccines.

The gene, designated, NXY, was isolated from a genebank produced from P. falciparum cells (K1 isolate) screened with antiserum obtained by immunising rabbits with P. falciparum isolate NF54. See also AAQ13728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antimalarial polypeptide(s) - corresp. to specific epitope(s) of the Plasmodium falciparum sporozoite antigen, and are useful as vaccines or to prepare antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-282989/39.
P-PSDB; AAR13991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1991;
                                                                                                                                                                                                                                                                 Sequence 3088 BP; 1375 A; 273 C; 575 G; 865 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN-LA ROCHE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1990;
                                                                    214 ttatggaaacatcagtagaaggaaatacaa 243
|| || || || || || || || || || ||
486 ctaggggcacatctgtacaaggacgcaaaa 515
                                                                                                                             Guttinger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90CH-0000970.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matile H;
                                                                                                                                                                                           Score 34; DB 12; Length 3088; Pred. No. 15; 0; Mismatches 35; Indels
                                                                                                                                                                                           0;
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WARN ANALE 39A9 SIHT

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
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                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                          Score
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XX Exal Yang F, 21-MAY-1998; 12-MAY-1999; 25-NOV-1999 WO9960160-A1 Homo sapiens Lung Specific Gene; LSG; human; diagnostic marker; prognosticate; lung cancer; diagnosis; ds. Human lung specific gene-3 27-MAR-2000 AAZ29726; AAZ29726 standard; (DIAD-) DIADEXUS LLC. 2000-116320/10. Macina RA, (first entry) 98US-0086212 99WO-US10344 DNA; Sun 895 BP

Example 1; Pages 35-36; 40pp; English.

A new method for diagnosing, monitoring and staging lung cancer

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                                                                                                                                                                                                                                                                       of a human Lng104 polypeptide
                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                  gene;
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ccctgtgatcatttcaagggcaatgtgaagaaaacaagacaccaaaggcaccacagaaag

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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human lung cancer specific gene (LSG), and encodes a polypeptide designated Lng104. LSGs are useful in the treatment and diagnosis of lung cancer. The treatment of lung cancer comprises the administration of a molecule which down regulates the expression of an LSG. An immune response can be mounted against a target cell expressing an LSG. Identification of potential therapeutic agents for use in imaging and treating lung cancer which comprises screening molecules for an ability to bind to or decrease expression of an LSG relative to LSG in the absence of the agent where the ability of a molecule to bind to the LSG or decrease expression of the LSG is indicative of the molecule being useful in imaging and treating lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New lung
cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                       Sequence
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ctgatgtccatggtctctagcagcctgaatccaggggtcgccagagggccacaggggaccga
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                                                                                                                                                                             acgctggcctgggactaaagcatagaccaccaggctgagtatcctgacctgagtcatccc
                                                                                                                                                                    acgctggcctgggactaaagcatagaccaccaggctgagtatcctgacctgagtcatccc
                                                                                                                                                                                                           2001-529917,
                                                                                  gcaccgacagttgcgatgaaagttctaatctcttccctcctcctgttgctgccactaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page
                                                                                                                                                                                                                                                                                                       1171
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                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                       B₽;
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RESULT
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ID AAZ9
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31-JUL-1998;
01-OCT-1998;
11-DEC-1998;
                                                                                                                                                                                                                                                   Lal P, T
Akerblom
                                         Claim
                                                                            New human signal peptide-containing prevention and diagnosis of e.g. car cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human signal peptide containing protein HSPP-94 cDNA
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DB; AAY87317.
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m IE,
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                                       Page 303;
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                                                                                                                                                                                                                                             Au-Young
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98US-0094983.
98US-0102686.
98US-0112129.
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H, Patterson
                                                                                           proteins useful in ncer, inflammation
                                                                                                                                                                                                                                    Guegler KJ,
on C, Reddy
                                                                                                                 useful in
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                                                                                             and
                                                                                                               treatment,
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                                                                                                                                                                                                                                  Baughn MR;
R, Hillman JL;
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В Qy

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cc human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, concluding cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders consisted with decreased activity or function of HSPP. Antagonists of contivity or function of HSPP. Such diseases include cell proliferation control of the control of the cell proliferation control of the control of the cell proliferation cell of the cell proliferation cell of the cell proliferation cell of the cell proliferation cell of the cell proliferation of the cell o
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P are also used to
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Sequence 870 BP; 244 A; 240 C; 177 G; 209 T; 0

Query Match Best Local :

95.9%;

Length

Qy 밁 Qy B Qγ DЬ Qy Д Qγ DЬ δÃ DЬ δÃ 밁 Qγ Ъ δÃ Вþ δÃ 뫄 QΥ 638 541 481 518 421 458 361 398 301 338 241 278 218 121 181 158 Local Similarity 100. hes 858; Conservative 61 38 cctgttctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctg cacctcactctcccactgtacccacccctaaatcattccagtgctctcaaaaagcatgtt aacaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttc aacaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttc gacaccaaaggcaccacagaaagccaaaccaggcattccagagcctgccagcaatttctca ctgggctgccaaagaagcagtgcccctgtgatcatttcaagggcaatgtgaagaaaacaa gacaccaaaggcaccacagaaagccaaacaagcattccagagcctgccagcaatttctca ctgggctgccaaagaagcagtgcccctgtgatcatttcaagggcaatgtgaagaaaacaa aagaatgtgagtgcaaagattggttcctgagagccccgagaagaaaattcatgacagtgt aagaatgtgagtgcaaagattggttcctgagagccccgagaagaaaattcatgacagtgt tcgccagaggccacagggaccgaggccaggcttctaggagatggctccaggaaggcggcc tcctcctgttgctgccactaatgctgatgtccatggtctctagcagcctgaatccagggg tattottcaagcaacttacagctgcaccgacagttgcgatgaaagttctaattctttccc agtatoctgacctgagtcatccccagggatcaggagcctccagcagggaaccttccatta 157 cctgttctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctg tcgccagaggccacagggaccgaggccaggcttctaggagatggctccaggaaggcggcc tcctcctgttgctgccactaatgctgatgtccatggtctctagcagcctgaatccagggg tattcttcaagcaacttacagctgcaccgacagttgcgatgaaagttctaatctcttccc agtatcctgacctgagtcatccccagggatcaggagcctccagcagggaaccttccatta 0, Score 858; DB 21;] Pred. No. 8.2e-259; Mismatches Indels 0 Gaps 697 637 600 540 577 480 420 457 397 337 180 60 360 300 240 120 97 0;

AAZ98109 to

AAZ98242

encode

AAY87224 to

AAY87357

which represent

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RESULT
ADA09257
ID ABAO
XX ABAO
XX ABAO
AC ABAO
AC ABAO
XX Huma
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which
                                                                                                                                                                                                                                              Tang
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27-APR-2000;
                                                                                                                                                                                               Claim
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mammalian subject
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Mismatches

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CC haematopoiesis regulatory activity; tissue growth activity;

CC immunomodulatory activity; activities; haemastatic, thrombotic or

CC chemotactic or chemokinetic activities; haemastatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC dispending on their biological activities, polypeptides and nucleotides of

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC immunomodulatory activities may be used in cell cultures to

CC polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness.
                                                     that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable activities, and hence potential therapeutic applications. The polypeptides of the invention makes various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, the
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                                                                                       The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques.
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KW PRO
KW dog;
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dog; cat; pig; gc
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                         DNA encoding
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goat; rabbit; tumour

mammal; tumour; cancer; human; cattle;

necrosis factor alpha;

horse; sheep; ha; TNF-alpha; sheep;

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Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammals include dogs, cats, cattle, horses, sheep,
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                                                                                                                     nucleic acids encoding PRO polypeptides, nice of tumours, such as prostate and break reen for modulators of the compounds -
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lung; breast; prostate; rectum; cervix; liver; genetic disorder;
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2000US-189328P
2000US-190828P
2000US-191007P
2000US-19100S
191314P
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192655P
2000US-193053P
2000US-193053P
2000US-194647P
2000US-194647P
2000US-195690P
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2000US-196820P
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2000US-19683P
2000US-19654P
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2000US-US13705
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ilarity 100.0%;
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18-FEB-2000
18-FEB-2000
01-MAR-2000
01-MAR-2000
03-MAR-2000
05-JUN-2000
05-JUN-2000
                                                                                                                                                                                                                   The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eaton DL,
Grimaldi
                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping.
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                 ctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctgagtatc 103
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DB; AAB87538.
ctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctgagtatc
                                                                               852;
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                                                                                              Similarity
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J, Gurney
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2000WS-0175481.
2000WO-US04341.
2000WO-US04342.
2000WO-US04614.
2000WS-0187202.
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2000WS-0193997.
2000WS-0214042.
2000WS-0214042.
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Pred. No. 6.3e-257;
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AC AAF4
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DT U2-A
DW Huma
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PRO842 (UNQ473) nucleotide sequence SEQ ID NO:164.

Human; secreted and to cell death; cancer; of diagnostic assay; ss. chromosomal mapping; transmembrane protein; gene mapping; tissue typing;

Homo

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Qy
                                                          Query Match
Best Local Similarity
                                          Matches
                                                                                                                                                                               sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAR44270 to AAR44470 represent PCR primers and hybridisation probes use in the isolation of human PRO sequences. AAR44407 to AAR65300 represent human PRO polynucleotide and protein AAR65194 to AAR65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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26-JUL-1999
28-JUL-1999
17-AUG-1999
17-SEP-1999
15-SEP-1999
08-CCT-1999
01-DEC-1999
01-DEC
                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
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Ferrara N,
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23-JUN-1999;
07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
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Roy MA, Stewart
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DB; AAB65191.
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2000WO-USO376.
2000WO-USO3765.
2000WO-USO4341.
2000WO-USO4914.
2000WO-USO4914.
2000WO-USO5004.
2000WO-USO50841.
2000WO-USO50841.
2000WO-USO5087377.
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Pong S, Gerber H, Gerritsen ME, Goddard
Gurney AL, Kljavin IJ, Napier MA, Pan
Wart TA, Tumas D, Watanabe CK, Williams
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99WO-US21547.
99US-0158663.
99WO-US28313.
99WO-US28301.
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99US-0146222.
99US-0149396.
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99US-0143048.
99US-0144758.
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99WO-US30911
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TGC-440 secretory protein nucleotide sequence

TGC-440; secretory protein; immunological disease; infectious disease; pulmonary function disorder; hepatic function disorder; nephrotropic; gastrointestinal function disorder; antiinflammatory; immunomodulatory virucide; hepatotropic; antiasthmatic; antibacterial; vaccine; immunomodulatory;

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RESULT AAC59829; AAC59829 11 standard; DNA; 654 ВP

secreted protein encoding DNA clone vq8

26-JAN-2001

(first

entry)

Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke; haematopoiesis regulation; tissue regrowth; wound healing; haemophilia; Alzheimer's disease; Parkinson's disease; Shy drager syndrome; cancer; ulcer;

contraceptive; psoriasis; ds. infection; growth inhibition;

sapiens.

WO200055375-A1

21-SEP-2000

17-MAR-2000; 2000WO-US07285

17-MAR-1999; 17-MAR-1999; 17-AUG-1999; 01-OCT-1999; 29-NOV-1999; 99US-0124808. 99US-0124916. 99US-0149639. 99US-0157247. 99US-0167824. 2000US-0182711.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for hyperproliferative disorders such as psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59494-7C95956. The proteins exhibit neuroprotective, dermatological, immunosuppressive,
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The present invention describes immunogenic portions of lung tumour-associated proteins (I) and the nucleic acids (NAs) that encode them. (I) have cytostatic activity and can be used in gene therapy, antiser

therapy, antisense

Claim

Page

186; 436pp; English

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RESULT 1
AAF68195
ID AAF6
AC CYL
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17-DEC-1999
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20-MAR-2000
10-APR-2000
10-APR-2000
27-APR-2000
05-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; lung cancer; lung tumour; lung tumo lung cancer antigen; lung tumour-specific cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                   WPI; 2001-071488/08
                                                                                                                                                                                                                                                                  Wang T,
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99US-0466867.

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tigen; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC inhibition and in vaccines. The NAs and the lung tumour-associated CC diagnosis of diseases associated with their inappropriate expression, CC especially lung cancers. For example, the NAs may be administered to CC treat diseases by rectifying mutations or deletions in a pattent's genome CC that affect the activity of the protein by expressing inactive proteins CC or to supplement the patients own production of (I). Additionally, the CC NAs may be used to produce the lung-tumour associated protein, according CC to standard recombinant DNA methodology. Conversely, antisense NA CC molecules may be administered to down regulate protein expression by CC binding with the cells own genes and preventing their expression. The NA CC and complementary sequences may also be used as DNA probes in diagnostic CC assays to detect and quantitate the presence of similar NA sequences in CC cancer. The (I) may be used as antigens in the production of antibodies CC expression and activity of the protein. AAF68083 to AAF68878 and CC AAB76878 represent human lung tumour protein related CC cucleotide and protein sequences which are used in the exemplification CC of the present invention.
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Best Local
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Secreted protein; gene therapy; protein therapy; diagnosis; treatment central nervous system; CNS; immune system; cancer; trauma; liver; reproductive disorder; congenital malformation; degenerative disease; inflammatory disease; neoplasia; metabolic disorder; testis; placenta brain; T cell; spleen; lung; heart; rhabdomyosarcoma; endocrine systems of the content of
                                                                            testis; placenta; endocrine system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment;
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Ното sapiens

endocrine endocrinopathy;

ophthalmopathy;

endocrine polyglandular syndrome; endocrinoma; seps: almopathy; osteoclastoma; bacterial infection; bone;

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08-APR-1997;
08-APR-1997;
08-APR-1997;
30-MAY-1997;
30-MAY-1997;
                                                                                    08-APR-1997;
08-APR-1997;
                                                                                                                                      07-APR-1998;
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                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                               sig_peptide
                                                                                                               30-MAY-1997
                                                                                                                                                             15-0CT-1998
HUMAN
GENOME
                       97US-0042825.
97US-0048068.
97US-0048070.
                                                            97US-0042726.
97US-0042727.
97US-0042728.
97US-0042754.
                                                                                                             97US-0048184
                                                                                                                                    98WO-US06801
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311..424
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/transl_except= (pos:383..385,
/note= "Xaa = unknown"
233..310
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/product= "secreted
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(HUMA-)

Feng P, N. J, Rosen CA, Ruben , MS Υu 6

P-PSDB; 1998-594496/50. DB; AAW83938.

bacterial infections New isolated human genes useful for the diagnosis disorders, immune system and secreted polypeptide(s) they encode and treatment of e.g. cancers, CNS disorders, inflammatory disease and

Claim 4. Page 107; 142pp; English.

The invention relates to 20 novel genes and their fragments (AAV69611 to AAV69630) and corresponding secreted proteins (AAV63931 to AAW83950) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein of gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of central nervous system (CNS) and immune system diseases, reproductive disorders, concerts, congenital malformations, degenerative diseases in testes, placenta, liver, brain and activated T cells, spleen diseases in testes, placenta, liver, brain and activated T cells, spleen This sequence represents a nucleic acid molecule designated Gene 8 from the human cDNA clone HIHCM89 (deposited as clone ATCC 97955 and ATCC 209074) which encodes a secreted human protein. This gene is expressed primarily in lung and to a lesser time pancreatic carcinoma and gall bladder and is useful as reagents for differential identification of tissues in a biological sample. endocrine system or heart diseases, endocrinopathies, endocrine Gene 8 from

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RESULT 1
AAX40454
AD AAX40
AD AAX4
AX AAX4
AC AAX4
AC AAX4
AX AAX4
AX Huma
AX Huma
XX Huma
KW Huma
KW Gore
KW Upst
KW Gore
KW Core
KW Core
KW Huma
KW Hore
KW Hore
KW Hore
KW Hore
XX Home
AX 
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Best Local S
Matches 466
                                                                                                                                                                                                                                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                              01-AUG-1997;
                                                                                                                                                                                                                                              reproductive hormone regulation; chemotactic; chemok thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                 31-JUL-1998;
(GEST ) GENSET
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX40454 standard;
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                                                                                 98WO-IB01232
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97.98;
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No. 2.6
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Query Match Best Local

Similarity

40.5%;

Score Pred.

362.4; No. 2.1

.1e-103; DB

20;

Length

0;

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common secreted proteins expressed in prostate, and encode the proteins of given in AAY1176 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The conclete acid sequences can be used for products for diagnosis and continuity. The proteins obtained may have cytokine activity, cell contiferation and differentiation activity, reproductive hormone continuity, tissue growth regulating activity, reproductive hormone continuity, the activity, respector/ligand activity, haemastopoiesis regulating activity, the activity, respector/ligand activity, haemastopy concluded activity, the continuity and continuity, and continuity activity. The products concluded in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter continuity extracellular secretion of a polypeptide can be used for of a polypeptide can be used for concluded into a membrane, or importing a polypeptide into a cell.
    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-153780/13.
P-PSDB; AAY11732.
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                                                                                                                                                                                                                                                                                                                                                                                                         1;
  365 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                     Page 185; 675pp; English.
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91 A; 100 C;
                                                                                                                                                                                                                                                                                                                                                                 represent
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96 G;
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78
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T; 0 other;
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te, and encode the proteins
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                         ctgttctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctga
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                                        standard;
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                                       DNA;
                                       BP.
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30-JUN-2000

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Query Match
Best Local S
Matches 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and can be used in vaccines. TGC-440 and the polynucleotide sequence encoding it can be used to treat, prevent and diagnose immunological, lung, liver, kidney or gastrointestinal disorders and infectious diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia, pulmonary hypertension, and Helicobacter pylori infection. An antibody immunospecific for TGC-440 is also useful in the above treatment and diagnosis, and also for quantifying the amount of TGC-440 in a liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide; hepatotropic; antiastnmatic; ancourted hypertension; hepatitis; nephritis; influenza; asthma; pulmonary hypertension; neneumonia; Helicobacter pylori infection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human secretory protein designated TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory, viruside, hepatotropic, antiasthmatic and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory protein TGC440, antibodies to it and compounds promoting inhibiting its activity for diagnosis and treatment of diseases of immune system, lung, kidney, liver and intestinal system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itoh
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Search completed: September Job time: 7991 sec 16, 2002, 03:05:13

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Maximum Match 100%
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ALIGNMENTS

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REFERENCE
AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                 source
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI772722
BI772722.1
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
/ALDhest="DHIUB"
//Abhest="DHIUB"
//Abhest="DHIUB"
//note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5202801"
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                                                                                                                                                                                                         /clone_lib="NIH_MGC_122"
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Matches 908; Conserv
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                                                                     tgccca-tttccctcagcattgaccgtctggagtttgaccttctgtatcctgccatcaag
                                                                                                 TCCCGTGATCGAGGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGG
                                                                                                            tcccgtgatcga-ggcttccttcaatggcatgtatgcagacctcctgcagctggtgaagg
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1; Mismatches 29;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM1432 row: n column: 19
High quality sequence stop: 793.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 852)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc
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/db_xref="taxon:9606"
/clone="IMAGE:5173842"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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Pred. No. 1e-180;
0; Mismatches 3;
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           DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution i found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM11508 row: 1 column: 06 High quality sequence stop: 782.
                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
Unpublished (1999)
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                                                  aaaaccagctgtgtcccgtgatcgaggcttccttcaatggcatgtatgcagacctcctgc
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                                     AAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGC
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/clone="IMAGE:5202893"
/clone_lib="NHH_MGC_122"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11449 row: m column: 09
High quality sequence stop: 793.
Location/Qualifiers
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National Institutes of Health, N
Unpublished (1999)
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Tissue Procurement: Life Technologies, Inc.
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/db_xref="taxon:9606"
/clone="IMAGE:5180336"
/clone=lib="NIH_MGC_115"
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                             Mammalia, Eutheria; Primates; Catarrina, 1 (bases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: WGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 17
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Location/Qualifiers
/organism="Homo sapiens"
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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                                                                                                                                                                                    gggagagggagrggagcggggccgaggactccagcgtgcccaggtctggcatcctgcacttg
                                                                                                                                                                 GGGAGAGGAGGAGCCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCACTTG
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National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryonal carcinoma"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Glontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Glontech); Site_2: Sfil (ggccattatggcc);
/site_2: Sfil (ggccattatggcc);
/site_2: Sfil (ggccattatggcc);
/site_3: Sfil (ggccattatggcc);
/site_3: Sfil (ggccattatggcc);
/souble-stranded cDNA was prepared from cell line RNA. 5/
adaptor sequence: 5'-CACGGCCATTATGGCCC-3' and 3' adaptor
/sequence: 5'-ATTCTAGAGCCCGAGCGCGGCCACATG-dT(30)BN-3'
/(where B = A, C, or G and N = A, C, G, or T). Average
/insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
/contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
// Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                       Library."
a 271 c
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/clone_lib="NIH_MGC_61"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                   43.6%;
97.5%;
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REFERENCE
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
              Plate:
                     found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                   602558678F1 NIH_MGC_61 Homo sapiens
                                 cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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   quality sequence stop: 706.
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cccaatctagtgaaaaaccagct-gtgtcccgtgatcgaggcttccttcaatggca-tgt
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//Lisb_bost="DBIOB (Tl phage-resistant)"
//Lab_bost="DBIOB (Tl phage-resistant)
//Lab_bost="
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/organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:4696842"
/clone_lib="NIH_MGC_61"
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Pred. No. 2.6e-159;
1; Mismatches 10;
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National Institutes of Health, Mammalian Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, In
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                                                                                                                                                                             Conservative
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a 302 c 246 g 190 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
/clone="IMAGE:5176856"
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                                                                                                                                                                                          40.8%;
                                                                                                                                                                          Score 684.6; DB 10;
Pred. No. 6.4e-155;
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1 (bases 1 to 836)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian
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CONA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov plate: LLAM11436 row: o column: 05
                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                           Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                          OCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTG
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pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NHH_MGC Library."
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Location/Qualifiers
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/clone="IMAGE:5175388"
/clone_lib="NIH_MGC_115"
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Pred. No. 8.4e-152;
0; Mismatches 29;
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121

В Qy DЬ δÃ

102 62

Matches

648;

Conservative

Score 624.2; DB 10 Pred. No. 2.2e-140; 1; Mismatches 4;

DB 10;

660; 2;

Indels Length

Gaps

Local

Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONTECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                             144
                                                                                         /clone="IMAGE: 4703816"
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/clone_lib="NIH_MGC_77"
/lab_host="DH108 (Tl phage-resistant)"
/note="0rgan: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCAATG-GT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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98.9%;
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602569143F1 NIH_MGC_77 Ho
mRNA sequence.
BG540252
BG540252.1 GI:13532485
EST.
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                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InMAGE:4693619"
/clone="InMAGE:4693619"
/clone="InMAGE:470"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatgcc); 5' a
3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
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GGGCAGCCTGGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAA
                                                                  AAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACCACCAGCATCCT
                                                                                                                                                        aaaagtcatcaaagaaaagctgacacaggagctgaaggaccacaacgccaccagcatcct
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Plate: LLCM1378 row: p column: 24
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Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, In
CDNA Library Arrayed by: The I.N.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence
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/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgcteggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGGCGACATG-dT[30]BN-3' (Where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

00 a 287 c 237 g 187 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:4619399"
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Pred. No. 4.1e-139;
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?t1=&t2=qV0-BT0229-251
099-038-c01&t3=1999-10-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 620.
                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                   Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Cos Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S
                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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mRNA sequence.
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602150403F1 NIH_MGC_81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="BT0229"
/dev_stage="Adult"
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Pred. No. 7e-139;
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                                         ctgccgctgctcagtgccatgcgggaaaagccagccggagg-atccctgtgctgggcagc
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                                                                                                                                                                                        gccaccttgatccaagccaccctcagtcccactgcagttctcatcctcggcccaaaagtc
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                                                                                                                                                                                                                                                                                                             637;
                                                                                                                                                                                                                                                                                                                        Similarity
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Conservative

1;

Score 604; DB Pred. No. 1.7e. 1; Mismatches

DB 10; L.7e-135;

Length Indels

ω

Gaps

122

467 422

362 407 302 347 242 288 182 228 36.0%; 99.2%;

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 642)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
Plate: LLCM1136 row: e column:
High quality sequence stop: 640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
          141
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and 3' adaptor sequence:

5'-ATTCTMGAGGCCGAGGCGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palc Alto, CA)."

a 215 c 170 g 116 t
                                                                                                                                                                                                                                                             /lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: Sfi1 (ggcgoctcggoc); Site_2: Sfi1
(ggccattatggcc); 5' and 3' adaptors were used in cloning
ggccattatggcc); 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:4291561"
/clone_lib="NIH_MGC_81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1371 row: a column: 22
High quality sequence stop: 636.
Location/Qualifiers
1 640, Consortium/LLNL at:
Location/Qualifiers
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Mammalla; Butherla; Primates; Catarrhini;
1 (bases 1 to 640)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                Similarity
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BG482968.1 GI:13415247
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/clone_lib="NIH_MGC_77"

/lab_host="DHIOB (TI phage-resistant)"
/lab_host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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98.9%;
                                                                                                                 Score 598.8;
Pred. No. 3.1e
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ctccttcctggtgaac-gccttagctaagcaggtcatgaa 679
                                       GACGACTGAGGCCCAAGCCATCCGCATGGACACCAGTGCAAGTGG-CCCAGCCGCCT
                                                                                            | gacgactgaggcccaagccaccatccgcatggacaccagtgcaagtggccccacccgcct
                                                                                                                                                                 CATCCTCCAGCTGCAGGTGAAGCCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCC
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Search completed: September Job time: 3296 sec 16, 2002, 01:42:43

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on:
                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          Score
         Query
Match Length DB
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895
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ALIGNMENTS

KEYWORDS SOURCE ORGANISM RESULT 1
AX224644
LOCUS
DEFINITION
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Chen,S.Y., Sun,Y. and Macina,R.A.
Methods for diagnosing, monitoring, staging, imaging and treating
lung cancer via lung cancer specific genes
Patent: WO 0161055-A 2 23-AUG-2001; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens human. 245 þ /organism="Homo sapiens" /db_xref="taxon:9606" 250 c 183 g 21 217 t DNA linear PAT 10-SEP-2001

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Chen, S.Y., Sun, Y. and Macina, R.A. Methods for diagnosing, monitoring, stallung cancer via lung cancer specific gepatent: WO 0161055-A 6 23-AUG-2001; diapexus, Inc. (US)
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Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A. Goddwaki,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,
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                            gaggccaggcttctaggagatggctccaggaaggcggccaagaatgtgagtgcaaagatt
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ggttcctgagagccccgagaagaaattcatgacagtgtctgggctgccaaagaagcagt
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Sequence
AX062486
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 533)
                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                          wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R.,
Carter,D., Retter,M.W. and Mannion,J.
                                                                                                                                                                                                                                       Patent: WO 0100828-A 113 04-JAN-2001; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                  Compositions and
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                                                                                                                                  Conservative
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                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
154 c 113 g 11
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                                                                                                                                Score 525.8; DB 6;
Pred. No. 1.2e-152;
0; Mismatches 2;
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                                    aatgctgatgtccatggtctctagcagcctgaatccaggggtcgccagaggccacaggga
                                                                                                              tccccagggatcaggagcctccagcagggaaccttccattatattcttcaagcaacttac 176
CCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGA
          ccgaggccaggcttctaggagatggctccaggaaggcggccaagaatgtgagtgcaaaga 356
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Sequence 51
AX182041
AX182041.1
                                                                                                                                                                                             Similarity 97.1
94; Conservative
                                                                                                                                                                                                                                                                                           Patent: WO 0146697-A 51 28-JUN-2001; Millennium Predictive Medicine, Inc. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                         cancer
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1 (bases 1 to 626)
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 9.1e-137;
0; Mismatches 12;
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tccaattaaacattctcagccaagaagacagtgagcacacctaccagacacttttcttct
                                        CAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCT
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                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (30-JUN-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 30, 2000 this sequence version replaced gi:7711512.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (07-OCT-1999) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
3 (bases 1 to 168586)
DOE Joint Genome Institute and Stanford Human
                                                                                                                                                                                                                                                                                                                   www-shgc.stanford.edu
Quality: Phrap Quality >-40 100% of
Estimated Total Number of Errors is
Location/Qualifiers
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 168586)
DOE Joint Genome Institute and
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AC011497.6 GI:8844110
                                                                                                                                                                                                                                                                                                                                                                                       www.jgi.doe.gov
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
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/clone="CTB-50E14"
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                                                                                                                                                  Score 438.4; DB 9;
Pred. No. 6.1e-125;
0; Mismatches 1;
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CTB-50E14, complete sequence.
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Creek, CA 94598, USA
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                                                                                                                     TTTGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTATTCCAATTAAACATTCTCAGCCA
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                                                                             AGAAGACAGTGAGCACCTACCAGACACTCTTCTTCTCCCACCTCACTCTCCCACTGTA
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AX332462.1
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Young, P.E., Augustus, M., Carter, K.C.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therape
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Location/Qualifiers
1. .419
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                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
63 c 117 g 11
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Pred. No. 5.2e
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Best Local Similarity
Matches 357; Conserv
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Novel protein and process for producing it
Patent: JP 2000139479-A 1 23-MAY-2000;
TAKEDA CHEM IND LTD
OS Homo sapiens (human)
PN JP 2000139479-A/1
PD 23-MAY-2000
PF 02-SEP-1999 JP 1999248414
PR VASUAKI ITO, KAZUHIRO OGI, HIDEYUKI TANAKA, CHIEKO KITADA PC
C12N15/09, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00, PC
C12N15/09, A61K31/00, A61K31/00, A61K31/00, A61K31/00, PC
A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/00
PC A61K35/00, A61K48/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15
PC A61K35/00, A61K48/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15
PC A61K39/395, C12P21/08, (C12P21/02, C12R1:91), C12N15/00, A61K37/
PC A61K39/395, C12P21/08, (C12P21/02, C12R1:91), C12N15/00, A61K37/
PC Key Location/Qualifiers
FT Source //organism-'Homo sapiens (human)'.
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aagggcaatgtgaagaaaacaagacaccaaaggcaccacagaaagccaaaccaagcattcc
                                                        agatggctccaggaaggcggccaagaatgtgagtgcaaagattggttcctgagagccccg
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Novel protein and proce
E40581
E40581.1 GI:18625110
JP 2000139479-A/1.
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A61K45/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,
G01N33/50//
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Location/Qualifiers
1. .357
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/db_xref="taxon:9606"
1 92 c 90 g 7
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                                                  E40584.1 GI:18625113
JP 2000139479-A/4.
                                                                            E40584 Novel protein and process
                                  Homo sapiens
                                        Homo sapiens.
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AX062416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases_1 to 312)
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/db_xref="taxon:9606"
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43 from Patent WO0100828
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100.0%; Pred. No. 6e-86;
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Novel protein and process for producing it

Patent: JP 2000139479-A 4 23-MAY-2000;

TAKEDA CHEM IND LTD

OS HOMO Sapiens (human)

PN JP 2000139479-A/4

PD 23-MAY-2000

PF 02-SEP-1999 JP 1999248414

PP 02-SEP-1999 JP 1999248414

PP 23-MAY-2000

PF 02-SEP-1999 JP 1999248414

PP 1 199248414

PP 1 23-MAY-2000

PP 02-SEP-1999 JP 1999248414

PP 1 23-MAY-2000

PP 02-SEP-1999
Eukaryota; Metazoa; Chordata; Craniata; Ve Mammalia; Eutheria; Rodentia; Sciurognathi 1 (bases 1 to 357)
Ito,Y., Ogi,K., Tanaka,H. and Kitada,C.
Novel protein and process for producing it Patent: JP 2001139479-A 3 23-MAY-2000; TAKEDA CHEM IND LTD OS Mus sp. (mouse)
PN JP 2000139479-A/3
PD 23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgccagcaatttctcaaacaatgtcagctaagaagctttgctctgcctttg
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                                                                                                                                                                                                                                                                      Mus sp
                                                                                                                                                                                                                                                                                         Mus sp.
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JP 2000139479-A/3.
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A61K45/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,
G01N33/50//
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Location/Qualifiers
1...291
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/db_xref="taxon:9606"
72 c 79 g 5
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s; Pred. No. 2.1e-79;
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s for pa
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E40582
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                                                                                                                       JOURNAL
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Best Local S
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PR
PI YASUAKI ITO, KAZUHIRO OGI, HIDEYUKI TANAKA, CHIEKO KITADA PC
C12N15/09, A61K31/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15
PC A61K45/00, A61K48/00, C07K14/47, C07K16/18, C12P21/02, G01N33/15
PC A61K39/395, C12P21/08, (C12P21/02, C12R1:91), C12N15/00, A61K37/
PC A61K39/395, C12P21/08, (C12P21/02, C12R1:91), C12N15/00, A61K37/
PC A61K39/395, C12P21/08, (C12P21/02, C12R1:91), C12N15/00, A61K37/
PT SOURCE 1, 357
FT SOURCE 1, 357
FT SOURCE 1, 357
1 (bases 1 to 357)
Ito,Y., Ogi,K., Tanaka,H. and Kitada,C.
Novel protein and process for producing it
Patent: JP 2000139479-A 2 23-MAY-2000;
TAKEDA CHEM IND LTD
OS Rattus sp. (rat)
PN JP 2000139479-A/2
PD 23-MAY-2000
PF 02-SEP-1999 JP 1999248414
PR
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                                                                                                                                                                                                                                                                         Novel protein and process f
E40582.1 GI:18625111
JP 2000139479-A/2.
Rattus sp.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                           Rattus sp.
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G01N33/50//
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/db_xref="taxon:10095"
103 c 92 g
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Pred. No. 3.3e-65;
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Sciurognathi; Muridae; Murinae;
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C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K35/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/1:
PC G01N33/50/
PC A61K39/395,C12P21/08,(C12P21/02,C12R1:91),C12N15/00,A61K37/
PC A61K39/395,C12P21/08,(C12P21/02,C12R1:91),C12N15/00,A61K37/
PC Key Location/Qualifiers
FT Source //organism='Rattus sp. (rat)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                       aagggcaatgtgaagaaaacaagacaccaaaggcaccacagaaagccaaaccaagcattcc
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                                                                                                                                                                                                                                                     Mus sp.
PI YASUAKI ITO,KAZUHIRO OGI,HIDEYUKI TANAKA,CHIEKO KITADA PC C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,
                                                                                                                                 Novel protein and process Patent: JP 2000139479-A 6 TAKEDA CHEM IND LTD
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 291)
Ito,Y., Ogi,K., Tanaka,H. and Kitada,C.
Novel protein and process for producing it
Patent: JP 2000139479-A 6 23-MAY-2000;
                                                                                                                                                                                                                                                                                                      E40586
E40586.1 GI:18625115
                                                                                                                                                                                                                                                                                        JP 2000139479-A/6.
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                                                                Mus sp. (mouse)
JP 2000139479-A/6
23-MAY-2000
02-SEP-1999 JP 1999248414
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A61K45/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,
G01N33/50//
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Location/Qualifiers
1..357
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/db_xref="taxon:10118"
101 c 93 g
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                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaattcatgacagtgtctgggctgccaaagaagcagtgcccctgtgatcatttcaagggc 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTGGAAGGTGGCCAAGAATGTGAATGCAAAGATTGGTTCCTGCAAGCCCCCAAAGAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCCGAACCCAGGGTCGCCAGAAGCCACGGGGACCAACACCTGGCTCCTAGGAGGTGG 60
Submitted (06-OCT-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. Cosmid F24866 overlaps cosmid R32065 to the left from bases 1 to 5,578 of this accession, and overlaps F13825 to the right from bases 35,645
                                                                                                                                                                             Lamerdin, J.E., McCready, P.M., Skowronski, E., Viswanathan, V., Burkhart-Schultz, K., Gordon, L., Dias, J., Ramirez, M., Stilwagen, S., Phan, H., Velasco, W., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Reller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Saunders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V., Suguence analysis of a 2.5 Mb region in 19q13.2 containing a clustered CEA/PSG gene family
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                                                                                                              2 (bases 1 to 44332)
Lamerdin, J.E.
Direct Submission
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AC005794.1
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34; Conservative
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immalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A61K38/00,
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Location/Qualifiers
1. .291
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/db_xref="taxon:10095"
82 c 80 g
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                                                                                                                                                     /note="BLASTX similarity to (151. .233); match: 0. score: 4.2e-23; database searched: nr; biliary glycoprotein h precursor - human gi|179435 (M69176) biliary glycoprotein a [Homo sapiens] >gn1|PID|d101 (D90312)
   glycoprotein i precursor
                                       score: 4.7e-23; database
                                                                          complement(15573...15821)
/note="BLASTX similarity"//
/note="BLASTX similarity"//
/note="blast"/
/note="bl
                                                                                                                                                                                                                                                                                                                                             /rpt_family="MSTA" complement(15573.
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13161.
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complement(6739. .7153)
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complement/0010
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complement/070"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alusx"
13613. .13831
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13331. .13604
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7570. .7673
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 84.000"
complement(join(<1522. .1880,2814. .2974))
/product="Human CGM7 gene for nonspecific cross-reactiantigen (NCA)"</pre>
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2063. .2382
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complement(join(<1522..1880,2814..2877))
/genpe="CCM7"
/note="NCA"
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/gene="CGM7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /...ap="19q13.2 between BCKDHA and D19S217"
/clone="F24866"
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/db_xref="taxon:9606"
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                                                                                                                                                                                [Homo sapiens] >gnl|PID|d1015048
                                   to (151. .233); matc searched: nr; biliary
human gi|179437
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                                                                  match: 0.57
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/rpt_family="MER4_internal"
complement(25088. .25368)
/rpt_family="MER57_internal"
complement(25389. .25768)
/rpt_family="MER57_internal"
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complement(21173, .21261)
/rpt_family=""AluJb"
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/note="BLASTX similarity to 437784 (3. .34); match: score: 7.2e-08; database searched: nr; (Z21818)  
carcinoembryonic antigen [Homo sapiens]"
                                              /note-"BLASTX similarity to Q13946 (65. .100); match: 0.63 score: 5.0e-30; database searched: nr; HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (HCP1)"
                                                                                                          26147. . 26317
/note="BLASTX similarity to Q13946 (7. .63); match: score: 5.0e-30; database searched: nr; HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (HCP1)"
                                                                                                                                                                                                                                                                                 frame: 1, quality: good, score: complement(23278, 23613)
/rpt_family="LTBR"
complement(23863, 24002)
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/note="BLASTN similarity to M87707 (105. .204); match: 1, score: 6.2e-3; database searched: nt; Human simple repeat polymorphism."
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complement(20324. ...
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/note="predicted exon, program:
frame: 2, quality: good, score:
15889 .16138
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/note="BLASTX similarity to 37204 (248.
score: 1.0e-06; database searched: nr;
protein [Homo sapiens]"
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/rpt_family="(CA)n"
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(D90313)"
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complement/corr
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KEYWORDS
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1 (bases.1 to 291)
Ito,Y., Ogi.K., Tanaka,H. ar
Novel protein and process fc
Patent: JP 2000139479-A 5 23
TAKEDA CHEM IND LTD
OS Rattus Sp. (rat)
PN JP 2000139479-A/5
PD 23-MAY-2000
PF 02-SEP-1999 JP 19992484
PR
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JP 2000139479-A/5.
Rattus sp.
Rattus sp.
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Novel protein and process
E40585
                                                                                                                                                           Rattus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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28652. .30135
/rpt_family="L1"
complement(30136. .30213)
/rpt_family="THE1A"
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complement(41469. .42015)
/note="BLASTN similarity to AQ108164 (2. .548); match:
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complement(39711. .40104)
/rpt_family="LTR8"
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source
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A61K45/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,
G01N33/50//
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Location/Qualifiers
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/db_xref="taxon:10118"
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Search completed: September 16, 2002, 02:58:21 Job time: 7714 sec

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Chen,S.Y., Sun,Y. and Macina,R.A.
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                                                                                                                    tch 53.0%; Score 474; DB 6; L al Similarity 100.0%; Pred. No. 1.6e-261; 474; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     AX182041
Sequence
AX182041
                                                                                                                                                                                         Patent: WO 0146697-A 51 28-JUN-2001;
Millennium Predictive Medicine, Inc.
Location/Qualifiers
1. .626
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Mammalia; Eutheria; Pri
1 (bases 1 to 626)
Lillie,J., Palermo,A.,
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/db_xref="taxon:9606"
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AACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCCACTCTTC
                aacaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttc
                                                                    gacaccaaaggcaccacagaaagccaaacaagcattccagagcctgccagcaatttctca 517
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                                                    GACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCA
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                                                                                                                                                                                                                                                                                                                                                            Submitted (30-JUN-2000) DOE Joint Genome Institute, 2800 Morive, Walnut Creek, CA 94598, USA On Jun 30, 2000 this sequence version replaced gi:7711512. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459
3 (bases 1 to 168586)
DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                Quality: Phrap Quality >=40 100% Estimated Total Number of Errors Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
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Homo sapi
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DOE Joint Genome Institute.
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                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTB-50E14"
a 43600 c 40989 g 39515
                                                                                                                                                                                                                                                                         1. .168586
                                                                                                           48.9%; sc.
100.0%; Pr
                                                                                                               Score 438; DB 9; L
Pred. No. 7.7e-241;
0; Mismatches 0;
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GAGGCCAGGCTTCTAGGAGATGGCTCCAGAAAGGCGGCCAAGAATGTGAGTGCAAAGATT 180

gaggccaggcttctaggagatggctccaggaaggcggccaagaatgtgagtgcaaagatt 358

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TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCCACAGGGACC

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Sequence 113 pax062486
                                                                                                                                                                                                       Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S. Carter,D., Retter,M.W. and Mannion,J. Compositions and methods for the therapy and diagnosis of J
                                                                                                                                                                             Patent: WO 0100828-A 113 04-JAN-2001; CORIXA CORPORATION (US)
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 533)
                                                                              Similarity
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/db_xref="taxon:9606"
154 c 113 g 11
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agatggctccaggaaggcggccaagaatgtgagtgcaaagatttggttcctgagagccccg
                                        tctagcagcctgaatccaggggtcgccagaggccacagggaccgaggccaaggcttctagg 315
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                           TCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGG
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                                                                                                                                       357;
                                                                                                                                                                                                                                                                                         Patent: JP 2000139479
TAKEDA CHEM IND LTD
OS HOMO Sapiens (hu
PN JP 2000139479-A)
PD 23-MAX-2000
PF 02-SEP-1999 JP 1
PR YASUAKI ITO,KAZU
C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K48
PC A61K31/00,A61K48
PC A61K45/00,A61K48
PC A61K45/00,A61K48
PC A61K45/00,A61K48
PC A61K39/395,C12P2
CC KEY
FT SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ito,Y., Ogi,K., Tanaka,H. and Kitada,C. Novel protein and process for producing Patent: JP 2000139479-A 1 23-MAY-2000;
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JP 2000139479-A/1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
JP 2000139479-A/1
23-MAY-2000
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                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                               A61K39/395,C12P21/08,(C12P21/02,C12R1:91),C12N15/00,A61K37/02
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                                                                                                                                                                                                                                                                           /organism='Homo sapiens
                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
92 c 90 g 7
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Pred. No. 5.2e-194;
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Best Local Similarity 99.8
Matches 416; Conservative
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Sequence 297
AX332462
AX332462.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young, P.E., Augustus, M., Carter, K.C., Ebna Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic
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Location/Qualifiers
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2971 from Patent WO0194629
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/db_xref="taxon:9606"
63 c 117 g 11
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2.3e-170;
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 291)

Ito, Y., Ogi, K., Tanaka, H. and Kitada, C.

Novel protein and process for producing it

Patent: JP 2000139479-A 4 23-MAY-2000;

TAKEDA CHEM IND LTD
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Sequence 43
Ax062416
Ax062416.1
                                                                                                      Homo sapiens
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                                                                                                                            JP 2000139479-A/4.
                                                                                                                                        E40584.1 GI:18625113
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Patent: WO 0100828-A 43 04-JAN-2001;
CORIXA CORPORATION (US)
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Compositions and methods for the therapy and diagnosis of lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
1 (bases 1 to 312)
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                                                                                                                                                                protein and process
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llarity 100.0%; Pred. No. 4.7e-168;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
82 c 69 g 6
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PN JP 2000139479-A/4
PD 23-MAY-2000
PF 02-SEP-1999 JP 1999248414
PF 02-SEP-1999 JP 1999248414
PF 02-SEP-1999 JP 1999248414
PR PI YASUAKI ITO, KAZUHIRO OGI, HIDEYUKI TANAKA, CHIEKO KITADA PC C12N15/09, A61K31/00, A61K31
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Sequence 12
AX182077
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                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97)
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G01N33/50//
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                      /organism="Homo sapiens"
/db_xref="taxon:9606"
16 c 37 g 2/
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/db_xref="taxon:9606"
72 c 79 g 5
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Sequence 1294 from Patent WO0142467.
AX185599
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68; Conserv
                                                       assessment, prevention, and therapy of cervical cancer Patent: WO 0142467-A 1294 14-JUN-2001; Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
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                                                                                                                 Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 518)
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1 (bases 1 to 456)
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                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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PI YASUAKI ITO, KAZUHIRO OGI, HIDEYUKI TANAKA, CHIEKO KITADA PC C12N15/09, A61K31/00, A6
                                 AUTHORS
TITLE
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                                                            1 (bases 1 to 40520) DOE Joint Genome Institute and Stanford Human Genome Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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A61K45/00,A61K48/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                           40520 bp DNA linear PRI 21-APR-:
19 clone LLNLF-112E5, complete sequence
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c producing it.
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4.1e-11;
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                                                                                                                                                                                        Query Match 4.1%; Score 37; DB 9; Louis Local Similarity 100.0%; Pred. No. 1.7e-09; Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 40520)
DDE Joint Genome Institute.
Direct Submission
Submitted (07-0CT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 40520)
DDE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 21, 2000 this sequence version replaced gi:6015239.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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ALIGNMENTS

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Example 1; Pages 35-36; 40pp; English.
                                                                                   A new method for diagnosing, monitoring and staging lung cancer
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prognosticate; lung cancer; diagnosis; ds.
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                                                                                                                                                                                WPI; 2000-116320/10.
                                                                                                                                                                                                                                                                         Yang F,
                                                                                                                                                                                                                                                                                                                                                                 (DIAD-) DIADEXUS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1998;
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  ccaaacaagcattccagagcctgccagcaatttctcaaacaatgtcagctaagaagcttt
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01-OCT-1998;
11-DEC-1998;
                                               Claim
                                                                               New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovulatory defect;
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from natural sources.
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Matches 852
                                                                                                                                                                       sequences have homology with proteins including LDI receptors. THE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1998

18-AUG-1998

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                                                                                                                                                                                                                                                                      The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention without identified based on extracellular domain homology screening. The PR sequences have homology with proteins including LDL receptors, TIE
                                                                                                                                                 Sequence 870
                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                        Membrane-bound proteins
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Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR CC primers for PRO polypeptides of the invention. The sequences of the CC invention can be used to detect the presence of a tumour in a mammal by CR comparing the level of expression of a PRO polypeptide in a test sample CC of cells from the animal and a control sample of normal cells, whereby a CC higher level of expression in the test sample indicates the presence of a CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, CC pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TMF) alpha release from human CC blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The CC stimulate the proliferation or differentiation of chondrocyte cells. The CC susceptibility to tumour development, particularly adrenal, lung, colon, CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
            01-MAR-2000
02-MAR-2000
14-MAR-2000
14-MAR-2000
14-MAR-2000
15-MAR-2000
21-MAR-2000
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                                                                                                                                                                                                                                                                                                                    novel nucleic acids operation of tumours, to screen for model
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, Smith V,
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2000US - 201116P
2000WO-US13705
2000WO-US14941
2000WO-US15264
2000US - 2098129
2000US - 2098129
2000US - 0644848
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2000WO-US30952.
2000WO-US32678.
2000WO-US34956.
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2000US-199397P.
2000US-199550P.
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, Wood WI, Zh
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RESULT AAF92070 ID AAF9

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11-JAN-2000;
18-FEB-2000;
18-FEB-2000;
18-FEB-2000;
01-MAR-2000;
01-MAR-2000;
03-MAR-2000;
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15-SEP-1999;
07-DEC-1999;
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22-MAY-2000;
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                                                                                     ctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctgagtatc
tcaagcaacttacagctgcaccgacagttgcgatgaaagttctaatctcttccctcc
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DB; AAB87538.
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aldi CJ,
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J, Gurney AL,
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2000WO-US04341
2000WO-US04414
2000WO-US04611
2000WO-US05601
2000US-0187202
2000US-019397
2000US-019397
2000US-0209832
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99US-0170262.
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99WO-US21090.
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07-DEC-2000

02-JUN-1999; 30-MAR-2000;

99WO-US12252

2000WO-US08439

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                                                        WO200073454-A1
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07-JUL-1999
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17-AUG-1999
17-SEP-1999
17-SEP-1999
18-OCT-1999
30-NOV-1999
30-NOV-1999
30-NOV-1999
30-DEC-1999
30-DEC-1999
20-DEC-1999
20-DEC
                                                                                                                                                                                                                                                                                                                                                  sequences, and their fragments, can be used as hybridisation probes, in the monosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PRC primers and hybridisation probes us in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
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DB; AAB65191.
tcaagcaacttacagctgcaccgacagttgcgatgaaagttctaatctcttccctcctcc
                                                                             ctgacctgagtcatccccagggatcaggagcctccagcagggaaccttccattatattct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sent invention describes human secreted and transmembrane PRO S. The PRO proteins have cytostatic activity. The PRO proteins used for targeted delivery of bioactive molecules, such as radiolabels or antibodies, that cause cell death. PRO nucleotide
                                                                                                                                                                                                                                          Similarity
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Stewart TA,
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ilarity 100.0%;
Conservative
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99WO-US30911
2000WO-US00376
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99US-0143048.
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Gerber H, Gerritsen ME, Goddard
AL, Kljavin IJ, Napier MA, Pan
Tumas D, Watanabe CK, Williams
                                                                                                                                                                                                                                                                                                                     237
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ABA09257

11-JAN-2002 (first entry)

Human TGC-440 homologue-encoding cDNA, SEQ ID NO:1033

RESULT ABACA SAN ABACA ABACA ABACA ABACA XX ABACA XX Huma KW Huma KW Haen haen KW Hoher KW Chrt KW Chr myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; Human; cytokine; cell proliferation; cell differentiation; gr. haematopolesis regulation; tissue growth; immunomodulator; accinhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic dis osteopathic; vasotropic; antiarteriosclerotic; ant; virucide; antibacterial; haematopoietic disorder; growth activin; factor;

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Best Local S
Matches 857
                                                                                                                                                                                                                                                                                                                           haematopolesis regulatory activity; tissue growth ractor activity; climbunomodulatory activity; activity or inhibin-related activity. CI immunomodulatory activity; activin- or inhibin-related activities; cc hemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be converted in oncogenesis, cancer cell proliferation or metastasis. Compending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or amellorating medical conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with abnormal fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to manifeld to the cell growth. For example, such polypeptides may be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autolmmune disease or accidental damage. The polypeptides and nucleotides may also be used in the disgnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 867-868; 1963pp; English
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27-APR-2000;
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cctgttctcgccctcaaatgggaacgctggcctgggactaaagcatagaccaccaggctg
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2000US-0560875.
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Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke; haematopoiesis regulation; tissue regrowth; wound healing; haemophilia; Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;

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CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic, cantibacterial, virucide, and fungicide activity. The proteins and cc nucleotide sequences are useful as nutritional sources or supplements cand in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, cand disorders such as multiple sclerosis, systemic lupus cerythmatosus, rheumatoid arthritis, and for treating myeloid or lymphoid cerythmatosus, rheumatoid arthritis, and for treating myeloid or lymphoid cerythmatosus, rheumatoid arthritis, and for treating myeloid or lymphoid cerythmatosus, rheumatoid arthritis, and for treating myeloid or lymphoid cerythera are also useful in compositions for bone, cartilage, tendon, ci ligament and/or nerve tissue growth or regeneration, for wound healing, ci such as replacement and in the treatment of wounds, inclsions cand ulcers. Other uses include in the treatment of wounds, inclsions cand ulcers. Other uses include in the treatment of wounds, inclsions cripheral nervous system and neuropathies such as Alzhelmer's and cripheral nervous system and neuropathies such as Alzhelmer's and cripheral nervous system and neuropathies such as Alzhelmer's and cripheral nervous system and neuropathies as a contraceptive, and for treating coagulation disorders such as a contraceptive, and for creating coagulation disorders such as haemophilias. The protein and concleotide sequences with cadherin activity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, cancer. Other parasites, for effecting bodily characteristics such as height, weight, hair colour, effecting bodily characteristics cycles or rhythms, effecting metabolism, catabolism, anabolism, anabolism, catabolism, sefections are alimination of distance for inhibiting the growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1999;
01-OCT-1999;
29-NOV-1999;
15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, proteins exhibit neuroprotective, dermatological, immunosuppressive,
                                                      processing, utilization, storage or elimination of dietary fat, protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for
                                       hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory, antianaemic, nootropic, antiparkinsonian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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arthritis,
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                                                          treating
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Query Match
Best Local Similarity
Matches 630; Conserv

70.4%; illarity 100.0%; Conservative

0;

Score 630; DE Pred. No. 1.4 0; Mismatches

4e-309; 21;

ВG

Length

654;

0

Gaps

0

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RESULT 1
                                                                                                                                                                                             TGC-440; secretory protein; immunological disease; infectious disease; pulmonary function disorder; hepatic function disorder; nephrotropic; gastrointestinal function disorder; antiinflammarcory; immunomodulatory virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                  30-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                  AAA08343
WO200014226-A1
                                                                                                                                 Homo
                                                                                                                                                                pneumonia;
                                                                                                                                                                               hepatitis;
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                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                              Helicobacter
                                                                                                                                                                                 nephritis; influenza;
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                        /product= "TGC-440"
/note= "secret
                                                                               Location/Qualifiers 220..579
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                                                                                                                                                              pylori
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                                protein'
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secretory protein TGC440, antibodies to it and compounds promoti inhibiting its activity for diagnosis and treatment of diseases immune system, lung, kidney, liver and intestinal system -
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The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC diagnosis of diseases associated with their inappropriate expression,
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC treat diseases by rectifying mutations of (I). Additionally, the
CC NAS may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC assays to detect and quantitate the presence of similar NA sequences in
CC cassays to detect and quantitate the presence of similar NA sequences in
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF6878 and
CC nucleotide and protein sequences which are used in the exemplification

AF6808 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
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06-MAR-2000; 2000US-0519642.
22-MAR-2000; 2000US-0533077.
10-APR-2000; 2000US-0546259.
27-APR-2000; 2000US-0564066.
05-JUN-2000; 2000US-0589184.
 nucleotide and of the present
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present invention
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Best Local Similarity
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gastrointestinal function disorder; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                           TGC-440; secretory protein; immunological disease; infe-
pulmonary function disorder; hepatic function disorder;
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                                                                                   /product= "TGC-440"
/note= "secret-
                                                                                                                                                                   Location/Qualifiers
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1. No. 1.6e-206;
1. No. 2;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human secretory protein designated TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory, virucide, hepatotropic, antiasthmatic and antibacterial activities, and can be used in vaccines. TGC-440 and the polynucleotide sequence encoding it can be used to treat, prevent and diagnose immunological, lung, liver, kidney or gastrointestinal disorders and infectious diseases, such as hepatitis, nephritis, infleenza, asthma, pneumonia, pulmonary hypertension, and Helicobacter pylori infection. An antibody immunospecific for TGC-440 is also useful in the above treatment and diagnossis, and also for quantifying the amount of TGC-440 in a liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secretory protein TGC440, antibodies to it and compounds inhibiting its activity for diagnosis and treatment of dimmune system, lung, kidney, liver and intestinal system
                                                                                                          AAX40454 standard;
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Human; secreted

protein;

EST;

expressed sequence

tag;

diagnosis;

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AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for C human secreted proteins expressed in prostate, and encode the proteins CC given in AAX11716 to AAX1193 respectively. The proteins given represent CC the signal peptide and an N-terminal fragment of a secreted protein. The CC nucleic acid sequences can be used for producing secreted human gene CC products. They can also be used to develop products for diagnosis and CC therapy. The proteins obtained may have cytokine activity, cell CC proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, haematopoiesis regulating CC activity, tissue growth regulating activity, haematopoiesis and CC regulating activity, receptor/ligand activity, anti-inflammatory CC activity, tumour inhibition activity or other activities. The products CC are be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter CC sequences. The nucleic acids encoding the signal peptides can be used for colvential entry in the insertion of a polypeptide or the insertion of a polypeptid
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Best Local :
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              271'
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                                                                                                                                                                                                                                                                                                                                      128
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    molecules may be administered to down regulate protein expression by binding with the cells own genes and preventing their expression. The NA and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in samples, and hence which patients may be in need of treatment for lung cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the protein. AAF68083 to AAF6878 and nucleotide and protein sequences which are used in the exemplification
                                                                                                                                                                                                                           associated proteins (I) and the nucleic acids (NAs) that encode them. (I) have cytostatic activity and can be used in gene therapy, antisense inhibition and in vaccines. The NAs and the lung tumour-associated proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the activity of the cancer.
nucleotide and protein sequences of the present invention.
                                                                                                                                                              that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (1). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2000;
22-MAR-2000;
10-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1999;
15-OCT-1999;
17-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                            The present invention describes immunogenic portions of lung tumour-
                                                                                                                                                                                                                                                                                                                                                                                 Claim
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05-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                         tumor-associated proteins and the nucleic ul for preventing, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
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; 2000US-0533077.
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301 actcttcttctc 312
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Score
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ALIGNMENTS

AL356798

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DEFINITION

Human DNA sequence from clone RP11-467B11 on chromosome 9, complete sequence.

ACCESSION

AL356798

VERSION

AL356798.18 GI:15795413

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118068)

AUTHORS

TITLE

JOURNAL

CB10 1SA, UK. E-mail enquiries; humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Sep 27, 2001 this sequence version replaced gi:14455883.

Where differences assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

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RESULT
AC025794
              DEFINITION
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, reverselement.
                                               AC025794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RP11-467B11 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-467B11 is at 118068 in this sequence. The true left end of clone RP11-208F1 is at 29578 in sequence. The true right end of clone RP11-29B11 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-467B11 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chr9
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/db_xref="taxon:9606"
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100.0%; Pred. No. 1.3e-62;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Jun 13, 2001 this sequence version replaced gi:8225449. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young, G., Zainoun, Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-6207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L8057
Center clone name: 62_0_7
Sequencing vector: M13; M7815; 45% of reads
Sequencing vector: Plasmid; n/a; 55% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 217695 bases at least 040
Consensus quality: 221726 bases at least 040
Consensus quality: 223337 bases at least 020
Consensus quality: 223337 bases at least 020
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                     Quality coverage: 8.2 in Q20 bases; agarose-fp Quality coverage: 8.0 in Q20 bas.

NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                            be preserved
                                                                                                                                                                as soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 219000; agarose-fp
Insert size: 223999; sum-of-contigs
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              1 15086: contig of 15086 bp in length
15087 15186: gap of 100 bp
15187 15923: contig of 737 bp in length
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16695 16794: gap of 100 bp
16795 17880: contig of 1086 bp in length
17881 17980: gap of 100 bp
17981 18579: contig of 599 bp in length
18580 18679: gap of 100 bp
18580 1869: gap of 100 bp
18580 19268: contig of 599 bp in length
19269 19368: gap of 100 bp
19369 20014: contig of 646 bp in length
20015 20114: gap of 100 bp
20015 20114: gap of 100 bp
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                                          /note="assembly_fragment"
21634. .22538
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20922. .21533
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16795. .17880
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18680. .19268
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17981. .18579
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Homo sapiens junctophilin 3 (JPH
AP429315
AF429315.1 GI:17646244
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 125020)
Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
              Nat. Genet.
21583737
                                                                                                                                                               Homo sapiens
1694876
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/note="assembly_fragment"
149156. .211213
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211314. .226399
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61920. .126287
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30388. .32661
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51232 c 50642 g
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23439. .24125
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126388. .149055
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26977. .28437
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25042. .25887
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/note="assembly_fragment"
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Pred. No. 5.6;
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                                                                                                    Human chromosome 14 DNA sequence BAC R-898B23 of library RPCI-
from chromosome 14 of Homo sapiens (Human), complete sequence
                    Homo sapiens
                                                                                                                                                 CNS018OW
   Eukaryota;
                                                                          AL109759.4
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Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWSHGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAGNGKYEGTWSNGLQDGYGTETYSDG"
29056 a 32731 c 30696 g 28283 t 4254 others
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complement(<36507. .>36887)
/gene="JPH3"
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/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
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/gene="JPH3"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                          GI:8176900
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R-898B23 of library RPCI-11
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1 (bases 1 to 201794)

Heiligra., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
Gyapay,G., Saurin,W. and Weissenbach,J.
Sequencing of the human chromosome 14
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                           Percentage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
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Quality coverage: 6.74x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summary Statistics
Assembly program: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.genoscope.cns.fr/Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: GS
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                                                   Conservative
                                                                                                                    dbSTS:STS52678
Identified using the e-PCR software
a 36481 c 35544 g 60693 t
                                                                                                                                                                  /note="matching EMBL:AA012815
RHdb:RH75590
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                                                                                                                                                                                                    Identified using the e-PCR software
                                                                                                                                                                                                                                         /note="matching EMBL:AA128898
                                                                                                                                                                                                                                                                /clone_lib="RPCI-11"
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/db_xref="taxon:9606"
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Mus musculus, clone RP24-196I15
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                                                                                      sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone.
                                             will be sequenced to completion.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record contains 84 individual
          the record
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Center clone na
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quenced to completion. In the event th is updated, the accession number will
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938: gap of 100
9589: corr
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7335: cr
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26795: contig
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gap of 100 b
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94: contig of 642 bp
gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtcagttgtgttgcctttgttgagtcccaccttatattcaagtaggtatgactacaaatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 totocacoacttaagtatatotottagagatotacagcotocotttaggggacatacaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCGGAATATTGTCTAACAAAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ttgaaaatagattgtcacacaataaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequence of Bovine Herpesvirus 4, a Bovine Rhadinovirus, and Identification of an Origin of DNA Replication J. Virol. 75 (3), 1186-1194 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine herpesvirus 4 long unique region, complete sequence
AF318573 AF271211
AF318573.1 GI:12802528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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1 (bases 1 to 1088
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Bovine herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (03-NOV-2000) Project
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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGTAASSDMCNLCQGKKPAVCINTLFYRLRDRFPPIITSHRRDPYIITGSVGMYNDLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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Query Match
Best Local Similarity
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CDS

gene

12.6%;

Score 39.6; Pred. No. 9.

DB 14;

Length 108873;

CDS

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CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGVANILQCLFGNNSNMTVEILYNFVNIPYSFT" 17297. .18577 /note="ORF 10; BORFB1; conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHFVKQHKTKSLLSTLLTAWLAKRKTIRKELANCDDGPMKTILDKQQLAIKVTCNSVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIYTPDRCPDIPIQFQTDIIPNGTVLKLLGKTQDGASVCVNVFQQMVYFYVLVPDGVN
LSYVIQQTLNGGVNKQTCKFSITQERKKILKEYDPSLYPVYKITLSAPTEINQLVGNL
TSCGCEVFESNVNASTRFIIDNKFSTFGWYSCSNPHPRISQRDSRTDLEFDCGLGDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MEFFNPYISKKKTDKRISCYDDPDKKTNPYCRLVPKCFKTPGTP
GVISITTTDTPVLFHQDKEYPIFTSGDHQRSYWSALKPTPAPIPPKDKLFFHYYDIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYNYYTQKLASLREDLDNTIDLNRDRLVKDLSEMMADLGDIGKVVVNTFSGIVTVFGS
IVGGFVSFFTNPIGGVTIILLLIVVVFVVFIVSRRTNNMNEAPIKMIYPNIDKASEQE
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FKDYKFVKTMDTNNISTLDTFLTLNLTFIDNIDFKTVELLYSETERKMASALDLETMFR
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LNCMOST I NET LEET VK FOR SHI RDGEVKY YKTNGGLE HOOMANEY LNLSEHT NUT I
LNCMOST I NET LEET VK FOK SHI RDGEVKY YKTNGGLET SMIHHI LEELTKTWGRED
ERNNKTIGHK SROKRSYDTKTFOGA KGLSTAQVOY AY DHLRTSMIHHI LEELTKTWGRED
KKDNLMWYELSK I NPVS YMAA I YGK PVA YKAMGDA FMV SEC I NVDQASVNII HKSMRTD
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SGELFRFDLDQTCPDTKDKKHVEG1LLVLKKNIVPY1FKVRKYRKIATSVTVYRGWSQ
                                                                                                                                                                                                                                                                                FLPLSLNQLINNYISFGLVQSIFELEDYAQCTAMLVQCRFPGITTPLEITPIHYTEFN
MPLFLFKTQNTIINSLSLSLAIIFMKEFCFGICSYISTAPBETIFPGHSLAHHLPS
TDQGHLTLSGQAIKCNMFYTYMYFAGPPSMQFFKMEHTMASGRGDLQDACVKGMVSV
IKNIMMEVVNPNGLYKVSVNITNPHKPDHIWITLKFTVMVKPTDLVLVSVLPSTTLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EISEIAKMAKIPARRYLTDGQQIRVFSCLLEAAKKEHFILPIPGAQKPGGYQGATVIN
PIPGFYNTPILVVDFASLYPSIIQAHNLCYSTMIQDQNLHLHHLKPDDYETFHLSTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="DNA polymerase"
/prote1n_id="AAK07928.1"
/db_xref="GI:12802536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFDPSPGNDTSETHQKYV"
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/protein_id="AAK07927.1"
/db_xref="GI:12802535"
                                                                                                                              complement(18848.
                                                                                                                                                              EDSMNVATLGENIIYSRCHLNLKSENTPSPMDTP"
                                                                                                                                                                                                           CGKVWNIYTDSEKILKPGETLNLKLKYTYTRGNESTKAVMFITGTNTNPMVTIEPTIW
LPMTPLQVTIKNPTNMIITIKKDLAIAACVPYYSTLEDRQPPASPSVYFNPQDLTITW
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/db_xref="GI:12802537"
/translation="MTSTLVEFSIEGWQVNICNGNIILMTNLKDIPVQGGYGMLVKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYYSDGLPYGFWKYIDYLNNSYAALATGKYSVESLTFSTELSRPFGEYKTTTLPHLTV
YRKIMSRNEELPQIHDRIPYYFIKGDQRGCKSDLAEDPTYVSQNKIPISVEIYFDKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLNTVAKHCMGTQKEDVTYKEIPSLFRSGEAGRARIGSYCVLDSVLVLDLLKYFMIHV
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                                                                                 /note="ORF Bo4; short ORF of immediate early transcript 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRYIGILSSDKLVMKGVDLIRKTACSFVQTTSKEILDLVLRDPEVKQAAQYLCRQAPA
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTTTTGTACTAATATCTCTCATGATGAAAATGGAATGTTGATTTTTGAACCAGACTG 49678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGTATG 49746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACTGTATTGATTATGGATTCATGCAAAGTCCCCTAGATGGAATTTTTTGGAGTGTCTCT 49618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGAGATGTGAGGGTATAGTCAAAAGTATATTAATCAATATAATTTATCCCAACACGCC 49558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tttgagaaatagaacaaatgaaatcagtttctccaccacttaagtatatctcttagagat 91
                                                                                                                                                                                                                                                                                                                                                                                           current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is not the entire insert of clone Y116ABA. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                           The true left end of clone Y116A8 is at 1 in this sequence. The true left end of clone T06A10 is at 54597 in this sequence. The start of this sequence (1. .106) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125;
                                               the specified clone.
                                                                                                                                                         sequence AF099926.
For a graphical representation of this sequence and
                                                                                                                                                                                                               The end of this sequence (54597. .54700) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                 neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jes@sanger.ac.uk or rw@nematode.wustl.edu
On Nov 15, 1999 this sequence version replaced gi:5832821.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (31-DEC-1998) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 ISA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail
                                                                                                                                                                                                                                                                     AL132846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C. elegans:
investigating biology. The C. elegans Sequent
Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available information.
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AL117205 Z98858
AL117205.2 GI:6425237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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               sections once,
This sequence is NOT necessarily the entire insert of ed clone. It may be shorter because we only sequence sections once, or longer because we arrange for a sma
                                                                                                                                     //wormbase.
                                                                                                                         .sanger.ac.uk/perl/ace/elegans/seq/sequence?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54700 bp DNA COSMID Y116A8A,
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                                                                                                                                                         its analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlap between neighbouring submissions.
                                                                      SPLQASSKPATEPLLRPESTRRASSSASSKPEVQTTIPTEIRTSSLPTPFLKTSTTVT
TTTPEPATVDYGDDHDMIGLDDEYGDESNKGVGKIDRIVGFFVLLLVIE*
complement(join(25359...25414,25792...26337,26389...26506,
                                                                                                                                                            /db_xref="STTREMBL:Q902W3"
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/translation="MKFQWITVTEKSGWLDTTSTSLETTIMQASSASTTSIKESTTTED
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/translation="MKFQWITVTEKSGwldtts"
/translation="MKFQWITVTEKSGwldttsike"
/translation="MKFQWldtsike"
/transla
                            26554. .26633,26676.
27279. .27402))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using Genefinder cDNA EST yk223al0.3 comes from this gene cDNA EST yk377c3.3 comes from this gene cDNA EST yk323al0.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:Q9U2W1"
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QSVPPGAVITEPAKKIIFNAPFDSMHTYQVKVINLSDRTIAYNIRTLNNKRFSIYPPC
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/db_xref="GI:5832825"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "INAOIAIHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Major sperm protein)
E-value=1.1e-15, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKKLIQLIACFFLLIPAASVFIRDPSFSSSSEEGYGRGKHHHGG
HHSPTPNPCEVGWYAFHRPQGVWCVKVVASKLTYLAAQTACINLGGALSGLQNDKERV
WIGNKOMEINLANGGTDSGTWLGAKCSSSGCTWTDGNTVGTQGMMFAPGEPNQLSYPP
CLYIWAKIGDTLKRYPYGNGYIDDTRLTTAMMSYACGKPGLRNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(22305.
23074. .231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GILKKTQNMFFNITFAPFNYTTENTKNDRITVKWINTPNNEDDEYFREWFHGDGMVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(12804. .13270,13318.
/gene="Y116A8A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Y116A8A.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(12804. .13270,13318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(4463. .4607,4651.
/gene="Y116A8A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB55164.1"
/db_xref="GI:5832827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains similarity to Pfam domain: PF00635 (MSP(Major sperm protein) domain), Score=64.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Y116A8A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB55165.1"
/db_xref="GI:5832828"
/db_xref="SPTREMBL:Q9U2W0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(4463. .4607,4651./gene="Y116A8A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mlhitansclighfidygskyflsftfsinilkscqiivfavnp
VNPVVASKLTYLAAQTACINLGGALSGLQNDKERVWIGNKGMEIMLANGGTDSGTWLG
AKCSSSGCTWTDGNTWGTQGMMFAPGEPNQLSYPPCLYIWAKIGDTLKRYPYGNGYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTRCTTAMMSYACGKPGLRNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB55161.1"
/db_xref="GI:5832824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Join(1517. .1562,1674. .1768,3071.
/gene="Y116A8A.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Y116A8A.1"
| join(1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="SPTREMBL:Q9U2W4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Y116A8A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05. .22428,22472. .22718,22764. .2
23153,23203. .23320,23373. .23929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1768,3071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4910,5667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4910,5667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3330,3372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3330,3372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .13360))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 22845, 22914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 22845, 22914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5876))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .3516)
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gene
                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains similarity to Pfam domain:
(Major sperm protein) domain), Score=61.1,
E-value=7.5e-15, N=1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAVKDERICTDTYKTEKAGGPLILNVSGKATVIGLKAPASRENCELFYDLSKLQKEIC
DYSGVCGHENPILTTEPTPVTTERSTVSTTISTSLETTIMQASSASPISSKPATTTEP
SPLQASSKPATEPLLQPESARTASSSASSKPEVQTTIPTEIQTPSLRTSSLKTSTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mkfqwigylvfigivnclissqkltvkeneerlkscgntflpipsingtgkgfgffinktytynsksgwlllaghknrstrvyatafpiseyhilissrvmltaehkwimngkpfdknncsggrhldvfpdvldnilfwygkkpkkadiskarwffacdn QDLkaypvlielnktssrpwaengvpcladettssklddvyhsygytgesmqheklsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
CDNA
                  E-value=1.9e-68, N=1
CDNA EST EMBL.214814 comes from this gene CDNA EST EMBL.214913 comes from this gene CDNA EST EMBL.84913 comes from this gene CDNA EST EMBL.84912.5 comes from this gene CDNA EST yk138a12.5 comes from this gene CDNA EST yk21633.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(31256...31363,31418...31531,31575.
31990...32269,32322...32376)
/gene="Y11688A.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:Q9U2V8"
/translation="mnnfLSICLRLLLFDFHDLFSTKNNDSAFLVSLTKRNTIPEYQS
VPPGAVITEPAKKIIFNAPFDSMHTYQVKVINLSNRTIAYNIRTLNMKRESIYPPCGI
                                                                                                                                                                                                                                                                                        complement(join(47919. .48041,49593. .50165,50969. 51584. .51908,52795. .52899,54267. .54318))
                                                                                                                                                                                                                                                                                                                                         WKSIEGCDGLDGFEFEDKFISKKGGYTWSDKNPDRLDNVQDCLVLWINPNDKEVDDDA
CGSNAKIKGFACGKEAG"
                                                                                                                                                                                                                                                                                                                                                                                 PKECOWCS IQNLMY IQKRESANNNMI IALKTDT INEITESVCTPFEQGIVNGNFNNTS
NLTQYKYSAQPSEDGNFLHFSYSAIKSCPSEWEPFDRIRGGWCIKVFRQGGSHDDAHR
ACKEYNAVLTRLETPKEMEYVWNTAYSVEAIFQKPSWEVYLETVWIDGVRKNECQVPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="predicted using genewise cDNA EST yk540c6.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Y116A8A.
/note="predicte
                                                                                                                                                                                                    51584. .51908,527
/gene="Y116A8A.9"
                                                                                                                                                                                                                           complement(join(47919. .48041,49593.
51584. .51908,52795. .52899,54267. .5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB55160.1"
/db_xref="GI:5832823"
/db_xref="SPTREMBL:Q9U2W5"
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/db_xref="GI:6425238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(29644. .29686,29735.
/gene="Y116A8A.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {	t TTTVTTTPDPATVDYGDDHDMIGLVDEDDEITESNNRAHRMDLILGQFEFFLSSFFT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB55163.1"
/db_xref="GI:5832826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(25359. .25414,25792. .26337,26389. .26506, 26554. .26633,26676. .26793,26862. .26943,26989. .27235,
                                                                                                                                                       (metallopeptidase family M24),
                                                                                                                                                                               /note="contains similarity to Pfam domain:
                                                                                                                                                                                                                                                                     /gene="Y116A8A.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MITHHRALMTCNSTEYSITETWRDCIELCAHNDSCVIAQTNLTV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Y116A8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(31256. .31363,31418. .31531,31575. .31728,31777.
31990. .32269,32322. .32376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lkktonme en it fapfnyttentkndr it vkwintpnneddey frewehgdgmynohh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(29644. .29686,29735. .30195)
/gene="Y116A8A.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:Q9U2W2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA EST yk82d6.5 comes from this gene NA EST yk290b7.3 comes from this gene NA EST yk2939e8.3 comes from this gene NA EST yk271a12.3 comes from this gene NA EST yk290b7.5 comes from this gene NA EST yk290b7.5 comes from this gene NA EST yk290b7.5 comes from this gene NA EST yk471a12.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted using Genefinder
comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .30195)
                                                                                                                                                          Score=239.2,
                                                                                                                                                                                                                           .54318))
                                                                                                                                                                                                                                              .50165,50969.
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Sequence split into 4 fragments LOCUS CEY113B8 Accession AL021573
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Sequence split into 4 fragments I Fragment Name Begin El CEY11388 0 1 21 CEY11388 2 200001 31 CEY11388 3 300001 31 COntinuation (2 of 4) of CEY11388 fi
102586 AAATTTCGAAAAATCAT 102570
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                                                                               AAGTCAAAAAATAAACCTCAATTAATGGATACTGGATGCAACGGAAATCTAAAGAAAATG 102587
                                                                                                                                                           TCTTTGAGTCAATTTTGCACATGTCTTAACATACTTTTGAAGTCATTATGTGATTTTGTA 102647
                                                                                                                                                                                                                                                                                                                      TCATGTTTTAATGAACATTTTTTTCCTAATTGATGAATTGGCCTTGATATTTAAAATAAA 102767
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                                                                                                    ttgtcacacaataaactggagtttatggaaacatcagtagaaggaaatacaacattccat
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CEY113B8_0
CEY113B8_1
CEY113B8_2
CEY113B8_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgcctttqttgagtcccaccttatattcaagtaggtatgactacaaattttgaaaataga
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                                                                                                                                                                                                                                Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                              * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                     OK 73019, USA
On Oct 30, 20
                                                                                                                                                                                                                                                                                                                 Submitted (31-JUL-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                     Ni,Y., Song,L. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
1 (bases 1 to 171179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG;
                                                                                                                                                                                                                         Center code: UOKNOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes clone rp43-111m15,
                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes BAC Clone rp43-111m15
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ni, Y., Song, L. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC092859.9 GI:16519522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unordered
                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                   as soon as it is available and the be preserved.
                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 171179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                              2001 this sequence version replaced gi:16445160
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2756: contig of 2756 bp in 2856: gap of unknown length 5886: contig of 3030 bp in 5986: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                      and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pan.
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                               208, Norman,
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KEYWORDS
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HSJ364H10/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 acttaagtatatctcttagagatctacagcctccctttaggggacatacaaagtcagttg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 gactcagattttaagaaataacttttgagaaatagaacaaatgaaatcagtttctccacc 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catccctttacagagatcatttacttgcaactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agattgtcacacaataaactggagtttatggaaacatcagtagaaggaaatacaacattc 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAATCCTGAAACGTTTCTAAAGCCAAGTTCTCATTGAAAGAATAAGCAAGTTTTCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATCCTGTAAGATTATAATGGAGCTGAAACAC 27205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGTCATATGCTGCATAACAATGTTTTGGTCAACAACAGGCTGCATAAATGTATGCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgttgcctttgttgagtcccaccttatattcaagtaggtatgactacaaattttgaaaat 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGGTAGAATTATTTAAGCTATCAATACTTGCAACTAAGATGTTATTAAAAAGGTAGGCA 27358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127;
                                                               Direct Submission
Submitted (21-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Nov 21, 1999 this sequence version replaced gi:5738453.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 150355)
                                                                                                                                                                                                                                                                                                                                                                 Contains STSs and GSSs, complete sequence. AL078603
AL078603.4 GI:6456827
                                                                                                                                                                                                                                    Williams, S.
                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA sequence from clone
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/clone_lib="RPCI-43"
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1. .171179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
/db_xref="taxon:9598"
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12377: gap of unknown length
20375: contig of 7998 bp in length
20475: gap of unknown length
37432: contig of 16957 bp in length
37532: gap of unknown length
60492: contig of 22960 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108413: gap of unknown 1
171179: contig of 62766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            150355 bp
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Pred. No. 9
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Mismatches
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5q16.1-16.3
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resolve all sequencing problems,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosome 6 Mapping Group. Furt
http://www.sanger.ac.uk/HGP/Chr6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP3-364H10 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-364H10 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         feature key.
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                                                                                                                                                                                                                                                                                                                                                                        /note="MER89 repeat: matches 1. .559
complement(16716 .17027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="34 copies 2 mer ag 89% conserved"
complement(8514. 9064)
                      /note="match: GSS: 29568. .30147
                                                            complement(29327
                                                                                                                                         /note="match:
24019. .24541
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/chromosome="6"
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                                                                            note="match: GSS: Em:B75442"
                                                                                                                                                                                             /note="10 copies 12 mer 69% conserved"
                                                                                                                                                                                                                                                                                                                note="match: STS:
                                                                                                                                                                                                                                                                                                                                                                                                                'note="MSTD repeat: matches 1. .394 of consensus"
15206. .15773
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                                                                                                                  'note="match: GSS:
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    GSS: Em:AQ322861'
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                                      Em: AQ279883"
                                                                                                                    Em: AQ310408
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                                                                                                                                                           Em: AQ240903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 4335. .4548 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .336 of consensus"
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/note="LIP repeat: matches 1601.
                                                                                                                                                                                                                                   /note="MLT2CB repeat: matches 459. 97891. .98411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62466. .62921
/note="MLT2B repeat: matches 4.
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/note="HERVL18 repeat: matches 5189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Tigger3b repeat: matches 1.
54775. .54811
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complement(40152. .40587)
/note="match: GSS: Em:AQ177754"
complement(40213. .40811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ008841" complement(71012 .71269)
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53699. .54781
complement(109446.
                      complement(109418.
/note="match: GSS:
                                                                          /note="match: GSS:
complement(109215.
                                                                                                                                                       /note="MER63A repeat: matches 2.
complement(101069. .101516)
                                                                                                                                                                                                                                                                           /note="MLT2CB repeat: matches 2. .448 of consensus"
93344. .93385
                                                                                                                                                                                                                                                                                                                                                          88350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75056. 75504
/note="LIMC1 repeat: matches 5653.
75929. .76148
/note="LIMC1 repeat: matches 6104.
78209. .78430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61258. .61598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Tigger3b repeat: matches 1069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30996. .31342
/note="MER58B
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MER58B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(74346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(70793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="LTR18A repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68053. .68404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Tigger3(Golem) repeat: matches 2298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Tigger3(Golem) repeat: matches 2861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49669. .49929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40819. .41341
                                                          /note="match:
                                                                                                                                                                                                                 /note="MLT2B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                    /note="4
                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:B88696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LTR16B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: STS: Em:Z79249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="HERVL18 repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LTR18A repeat: matches 1. .346 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1MA4A repeat: matches 6036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match: GSS: Em:AQ211747"
                                                                                                                                                                                                                                                                                                                    .93167
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                                                                                                                    .103031
                                                                                                                                                                                                 .100639
                                                                                                                                                                                                                                                                                                                                      copies 12 mer 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS: Em:B83962"
346. .74831)
                                                                                                                                    GSS: Em:AQ211414"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS: Em: AQ165687 **
                                      : Em:B56601"
.109858)
                                                                                              Em: AQ027024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Em: AQ307766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Em: B86714"
                    Em: AQ217743"
                                                                              ,109848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .444 of consensus"
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                                                                                                                                                                                                                 .448 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .337 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                .3701 of consensus"
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                                                                                                                                                                             .206 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .462 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6327 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5189 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6108 of consensus
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COMMENT

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JOURNAL REFERENCE
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AC011935
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ORGANISM
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                                                                                                                                                                                                                                                                                                              ACCESSION
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                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTTGTCAACTTAAGACCAAAAATTTGTGATTCATGTGTGGAAGGGATAAGAATATTA 101393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTGACTAAATTTCCTTTAAAACTTCTACTTCCTCCTAGGGTAAAATCTGAATTCTGTA 101513
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Olphuris...

2 (bases 1 to 168043)

2 (bases 1 to 168043)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Baldwin,J., Colatle,A., Collins,S., Collymore,A.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
                                                                                                                                            Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-16C5
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                               HTG;
                                                                                                                                                                                                                                                                                          AC011935
AC011935.4 GI:10198441
                                                                                                                                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                 (bases 1 to 168043)
                                                                                                                                                                                                                                                                         HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                           sapiens
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/note="match: GSS: Em:AQ310407"
complement(116724. .116977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121359. .121400
/note="21 copies 2 mer ct 81% conserved"
123140. .123710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="TIGGER2 repeat: matches 3. .2718 of consensus" 112200. .112686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="36 copies 2 mer tc 84% conserved" 121359. .121400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="111 copies 2 mer ga 64% conserved"
121253. .121324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="19 copies 12 mer 75% conserved"
120408. .120629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           consensus'
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complement(109700. .109858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LTR16B repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Tigger3(Golem)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="HERVL repeat: matches 5226. .5344 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="HERV16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match:
                                                                                                                                                                                                                                                                                                                                           168043 ; clone RP11-16C5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%; 50.8%;
                                                                                                                                                                                                                                                                           HTGS_DRAFT
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113936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat: matches 1929. .2435 of consensus"
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STS: Em:Z84791"
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                                                                                                                                                                                                                                                                                                                                           bp DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                                           DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150355;
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                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                            HTG
                                                                                                                                                                                                                    Euteleostomi;
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* 49699 : 56999: contig of 7301 bp in length
* 57000 57099: gap of 100 bp
* 57100 62962: contig of 5863 bp in length
* 62963 63062: gap of 100 bp
63063 74452: gap of 11290 bp in length
74453 88200
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Center clone name: 16_C_5

Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dbe; 100% of reads chemistry: Dye-terminator Big Dbe; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 159963 bases at least Q40 consensus quality: 16378 bases at least Q30 consensus quality: 16359 bases at least Q20 Insert size: 166443; sum-of contigs
                                                                                                                                                                                                104524: contig of 16224 bp
104525 104624: gap of 100 bp
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88300: contig of 13748 bp

88300: gap of 100 hr

104524: contir
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Homo sapiens clone RP11-492P1, c.
AC012075
AC012075.10 GI:13677160
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 185437)
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Similarity 45.8%;
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ne 10 clone RP11-76F14, complete
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                                                                                                                      p DNA linear complete sequence.
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                           Direct Submission
Submitted (21-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                      218939 bp DNA linear HTG 27 Homo sapiens chromosome 2 clone RP11-748B21, WORKING DRAFT SEQUENCE, 3 unordered pieces.
        9 M
                                                                                2 (bases 1 to 218939)
Waterston, R.H.
                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                 Waterston, R.H.
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 218939)
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                     AC079997.5 GI:18377352
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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On Apr 19, 2001 this sequence version replaced gi:11465168
Center project name: H_NH0492P01.
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Submitted (20-APR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (19-0CT-1999) Genome Sequencing Center, Washington University....
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The sequence of Homo sapiens clone
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/db_xref="taxon:9606"
/clone="RP11-492P1"
33701 c 33387 g 59270
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2002 this sequence version replaced gi:18129602
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Db 134673 CCATGAAAACAGATAGTTACACTGAGACTAAAAGACAATTGAAAGAACATTCAAATGAGA 134732
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Db 134733 TTCAACAATTTATACCTTTTAAG 134755
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Chemistry: Dye-terminator Big Dye; 50% of reads
Chemistry: Dye-terminator Big Dye; 50% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217808 bases at least Q40
Consensus quality: 218152 bases at least Q30
Consensus quality: 218152 bases at least Q30
Consensus quality: 218644 bases at least Q20
Insert size: 211000; agarose-fp
Insert size: 218739; sum-of-contigs
Quality coverage: 8.54 in Q20 bases; squrose-fp
Quality coverage: 8.53 in Q20 bases; sum-of-contigs
                              tacaacattccatccctttacag 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arritrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 48%
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/note="assembly_name:Contig24
clone_end:SP6
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24145, .84338
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/db_xref="taxon:9606"
/chromosome="2"
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Æ	AF19402	10	1668	٠	2.8	41	
AC	AC068495	N	174384	٠		40	•
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· AI	AB055896	10	1675	•		36	
AC1	AC107771	N	68591	٠	.2	35	.,
AL13	SCC	-	45335	•	4.2	34	
AF3	AF369213	9	336	•	4.4	33	
AF350	AF350278	w		•	4.6	32	()
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AF0	AF06	ш	3312	2.7	G	29	
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AL0	SC3C	Н	31382	2.7	σ	27	
AB0		4	1696	•	σ	26	
AC0	AC094	2	185005		8	25	()
AB0	AB033	9	5676		7	24	
AL3		ب	33285	•	7.8	23	
AF158745		9	1084		8.8	22	
всо		9	1053	•	8.8	21	
AB0	AB024937	9	1015	2.9	48.8	20	
E53		σ	1015	•	8.8	19	
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ALIGNMENTS

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Sequence 1 from Patent W00161055.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sequence 5 f
AX224647
AX224647.1
                                      Methods for diagnosing, monitoring, sung cancer via lung cancer specific Patent: WO 0161055-A 5 23-AUG-2001; diaDexus, Inc. (US)
                                                              Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 2036)
Chen, S.Y., Sun, Y. and Macina, R.A.
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1 586 c 528 g 44
                        Location/Qualifiers
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Query Match Best Local

Similarity

98.6%; 99.7%;

Score Pred.

1656.2; No. 0;

DB 6;

Length

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BAS	JO FEAT	H	REF	SOU	VER	RESULS AX092: LOCUS	рь	Qy	Db	Qy	ρ _δ	ОУ	Qу	Оy	ду Оу	Db Qy	Qу	ОУ	Qy Db
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REFERENCE AUTHORS TITLORS TITLORS JOURNAL REMARK COMMENT	RESULT 4 BC008429 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	09 1 0b 1		Qy 1 Db 1 Qy 1 Db 1	0		Db Oy
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCE 1 (bases 1 to 1684) Strausberg, R. Direct Submission NAL Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web Site: http://www-shgc.stanford.edu	BC008429 1684 bp mRNA Homo sapiens, Similar to DNA segment, Cl Institute of Technology 19, clone MGC:1/ Complete cds. BC008429 BC008429 1 GI:14250057 MGC.	.551 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAAT	150 gaaacccagctctcctgtctcccagtgaagacttggatggcagccatcagggaaggctgg	1430 gaaccagaatggcaaattaagatctggggtcccagtgtcattggtgaaggccttgggatt 1489	1310 acception and care coagetect partogrates acagete gradual terror partogrates and the coagete gradual terror partogrates and the coagete gradual terror partogram and the coagete gradual terror parto	yy-yy-coarcygacygyagytttocococagygaagocytcogocytttytt	

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This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.
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SHGSLRIQLLHKLSFLVNALAKOVMNLLVPSLDNLVKNQLCPVIEASFNGMYADLLQL
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TQIVKILTOOTPEEFIDOGHAKVAQLIVLEVPDSSEALRPLFTLGIEASSEAQFYKG
DQILLNINNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSL
VKALGFEAAESSLSKDALVLTPASLWRPTSPVSQ"
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/note="Vector: pDh
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M., Schmutz, J., Grimwood, J., Rodriquea
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                     276 catcotgcagcagotgcogctgctcagtgccgtgggaaaagccagccggaggatccct 335
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CATCCTCCAGGAGTTGCCACTGCTCAGAGCCATGCAAGATAAGTCTG--GCAGTATCCCC
                                                                              TGGCCCAGAAGTCATCCAGAAACACCTGACCCAGGCACTGAAGGACCATGATGCCACTGC
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Submitted (17-JAN-1996) Malcolm L. Snead, Center for Cranio Molecular Biology, University of Southern California, 2250 Alcazar St. Los Angeles, CA 90033, USA
On Aug 10, 2000 this sequence version replaced gi:1184789.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to.1629)
Snead,M.L., Villanueva,J., Paine,M.L., Lei,Y.P., Zhu,D.H.,
Lusis,J., Xia,Y.-R. and Yang,J.-N.
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ESTLRLSGLHKLSFYVWSLAKKVYMILLVPALPOJVKNHCLPMIQQAFDDMVEDELRTT
TAPIALSPGALEFGLLSPAIQDSNILLNLKAKLLDSQARVTNWFNNSATSLMETTPDG
APFSLTVRQDLVNAIVTTLVFREELVLLRFVIPVARQLQMDKSEINAEAANKLGPT
APFSLTVRQDLVNAIVTTLVFREELVLLRFVIPVARQLQMDKSEINAEAANKLGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="Swiss-Webster"
/db_xref="taxon:10090"
/chromosome="2"
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aacctg ATCCTG	CTTC	CCCtgggca	CCCAA	tgaag TGAAG	agtca AGATG	CAAG	111	GGTA	TATO	ccatc	tggt TGAC	ACCAC	CIC	90	gtgc	AAGC	- 0	CTGG	ctor	caggt	AC.	- ac
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cac 1	paac 1 ATC 1	aaa 1 GAA 1	IGCC 1	gac AAT	aag AAG	CCT	8-5	TG	AAG	- D	ggag GGAG	CATG	AGC -	atc	gcat TCAC	cacc	cac	AGTTC	CAG	caa	CI –	tcaca
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Burgess,C.E.,
Gusev,V.Y.
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                                                        Homo sapiens
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       Padigaru,M.,
Liu,X., Patt
                                    Hominidae;
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	COMMENT	TITLE JOURNAL	REFERENCE	io o	ACCESSION	RESULT 8 AL355392 LOCUS DEFINITION	Db 853 (1017	Db 793	733	Qy 897	Db 701	. Оу 837
Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Not. SNISSPROT; Tr:, TREMBL; W:, WORMPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence. The left end of clone RP1-37019 is at 62286 in this sequence. The true right end of clone RP1-37019 is at 62286 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least assembly was confirmed by restriction digest. RP5-118734 is from that provided in the sequence of the data seem of t	OK. E-mail enquiries: humquery@sanger.ac.uk Cione clonerequest@sanger.ac.uk 2001 this sequence version replaced gi:6982468	entre, Hinxton, Cambric	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AL355392.7 GI:10178502 HTG; CGI-05; CpG island; RYF3; SNT1; SNTA1; syntrophin. human. Homo sapiens	20q11.1-11.23 Contains ESTS, STSS, Contains the gene for novel proteins alivary gland protein, the gene for a novel protein and protein and component, complete sequence. AL355392 AL117331	AL355392 159440 bp DNA linear	CCAGAAGAATTCATGGTCCTGTTGGACTCTGTGGT 887	cagaaga		GACCAA			atcaagggtgacaccattcagctctacctgggggccaagttgttggactcacagggaaag 896

VECTOR: PCYPAC2

translation="MPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVLPESAH"

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/gene="dJ1187J4.1"

/note="match: CDNAs: Em:U46068

/note="match: CDNAs: Em:L45068

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Em:AW176327 Em:AW176325 Em:A1909965 Em:A1909964

Em:AA428580 Em:AW384405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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join(5758. .5867,7116. .7295,8242. .8295,8799.
9841. .9908,10729. .10774,11885. .11948,12794.
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join(<3408. 3471,5782. .5867,7116. .7295,8242. .8295,

8799. .8957,9841. .9908,10729. .10774,11885. .11948,

12794. .12870,15591. .15650)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match:
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/db_xref="taxon:9606"
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                                                                                                                      codon_start=1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Continues in Em:AL121901 as bA49G10.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .57 copies 2 mer ga 61% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15761)
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                                                                                                                                                                  .8957,9841. .9
.12870,15591.
                                                                                                                                                                                                                                                                                    similar to mouse von 2.)"
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                                                                                                                                                                                      .9908
                                                                                                                                                                  .15650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                21105...21680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(11631. .11769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALR
PLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIH
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                                           complement(39991.
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complement (40006.
                                                                                                                       /note="match: GSS: 39961. .40217
                                                                                                                                                                                                                              /note="match: 39763. .40037
                                                                                                                                                                                                                                                                                                                            complement(39266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="256 copies 2 mer ca 68% conserved"
14836. .14871
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS:
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                                                        .40409
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.18004)
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.39748)
                             .40172)
Em:AL185783"
.40317)
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21115)
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                                             Em: AQ596761"
                                                                           Em:G02503"
                                                                                        40169
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22968)
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KEYWORDS
SOURCE
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7115 GGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTC 7174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   929 octgacaatgcccaccctggacaacatcccgttcagcctcatcgtgagtcaggacgtggt 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        869 ggccaagttgttggactcacagggaaaggtgaccaagttggttcaataactctgcagcttc 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                      RP11-49G10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-49G10 is at 1 in this sequence. The true right end of clone RP11-49G10 is at 1 fals sequence. The true right end of clone RP1-733023 is at 27823 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing
                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Jun 5, 2000 this sequence version replaced gi:8017404. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission annotation to the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requests:
On Jun 5,
                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humguery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161593)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone RPI1-49G10 on chromosome 20 Contains a gene similar to bovine salivary protein BSP30.the LOC51297 gene murine von ebner minor salivary protein, a novel gene, a pseudogene similar to STAN-induced STAT inhibitor-2, a pseudogene similar to STAN-induced STAT inhibitor-2, a pseudogene similar to stativary gland protein, a novel gene, a similar to ribosomal protein L12, a putative novel transcript, ESTS, STSS, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracey, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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HTG; BSP30; CpG island; LOC51297; LUNX; RPL12; STAT-inhibitor.
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Pred. No. 2.2e-32;
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         and repeats;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              we submit sequences with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
                                      26979
                                                                                                                                             /note="match: GSS: Em:AQ395327" complement(23473. .23950) /note="match: GSS: Em:AQ727877" complement(23637. .23948)
                                                                                                                                                                                             /note="41 copies 2 mer ag 75% conserved" complement(21172. 21428) /note="match: GSS: Em:A0395327"
/note="match: 31882. .32061
                                                                      /note="match: 23955. .24456
                                                                                                           /note="match: 23950. .24355
                                                                                                                                                                                                                                                                                                                                                                        complement(20975.
                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: 18333. .18770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Tandem repeat, Forced join, Approximately 500 bases missing according to restriction digest." 16219. .16387
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/note="2 copies 60 mer 85% conserved"
complement(8476. .9002)
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                                                       note="match:
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                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AZ055779 Em:AZ084220"
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21031. .21263
                                                                                                                                                                                                                                                                                                                                                                                        /note="match:
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16225. .16387
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533. .686
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137. .548
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complement(1. .107)
/note="match: GSS: Em:AQ607627"
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15061)
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48787
                                                                                                                                                                                  /note="match: 53972. .54142
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52540. .53450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **Translation="MLQLWKLVLLCGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGLETVDNTLKGILEKKVDLGVLQKSSAWQLAKQKAQEAEKLLNWISKLLPTNTDIFGLKISNSLILDVKAEPIDDGKGLNLSFPVTANVTVAGPIIGQIINLKASLDLLTAVTIGTDPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFTHSLDYNVLQGCASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICPLIRIFTHSLDYNVLQQVVDNPQHKTQLQTLI"
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join(35535. .35585,36507. .36678,40308. .40452,41455. .4
42783. .42385,45523. .45604,46980. .47043,47896. .47973,
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33693...33;
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                                                                                                                                                                                                                                                                                                                                                                        complement(53844.
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complement(53831..54131)
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match: ESTs: Em:AI654622"
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                                                                                                              complement (54027
                                                                                                                                                                                                                                                             53958
                                                                                                                                                                                                                                                                                              complement (53908
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/db_xref="GI:9801234"
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                   /note="match:
                                                                                                                             54000. .54141
/note="match: GSS:
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48769. .48774
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.45604,46980. .47043,47896. .47936)
ba49G10.1"
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                                                                                                      Burch, P. Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howards, S., Huber, J., Hulk, S., Harlyk, S., Harlyk, S., Klan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Loulseged, H., Lozado, R.J., Lucker, A., Lucier, R., Luna, R., Man, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Miller, G., Miner, Z., Mitchell, T., Mohabbat, K., Moguen, M., Norris, S., Moser, M., Neal, D., Newtson, N., Newtson, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L.L., Peters, L., Sparks, A., Stanley, H., Sisson, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alie
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barba
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tahor,J., Taylor,T., Telfrod,B., Thomas,N. Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N. Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note="bA49G10.2 (similar to STAT-induced STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, C., Adio-Oduola, B., Ali-osman, F.R.,
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100.0%; Pred. No. 1.6e-27
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*** SEQUENCING IN PROGRESS ***,
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Barbaria,J.,
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                                                               Tamerisa, K.,
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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Wall,R., Wang,S., Ward-Moore,S., Warren,R., Watlington,S., Williams,G., Williamson,A., W Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zhou,J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbark_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Wleczyk,R., Wooden,S.,
Zorrilla,S., Nelson,D.,
       BASE COUNT
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                            Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Pred. No. 4.7e-09;
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of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, X 77030, USA On Dec 20, 2001 this sequence version replaced gi:15636607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 60 contigs. The true order of the pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GAHJ
Center clone name: CH230-3L3
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62896: contig of 1083 b
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Best Local Similarity

NOTE: This record contains 82 individual

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                                                                                                                                                                                  Research, 320 Charles Street, Cambridge, Marker: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-106C21
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Center project name: 10
                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome
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                                            Project Information
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LOW-PASS SEQUENCE SAMPLING.
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is useful.
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9954: contig of 720 bp
9954: contig of 750 bp
10804: contig of 750 bp
10804: contig of 750 bp
11644: contig of 740 bp
1744: 9ap of 100 bp
1744: 9ap of 100 bp
12458: contig of 714 bp
12458: gap of 100 bp
13290: contig of 732 bp
13390: gap of 100 bp
14120: contig of 730 bp
14120: contig of 730 bp
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5914: gap of 100 bp
16663: contig of 749 bp i
6763: gap of 100 bp
17506: contig of 743 bp i
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21703: contig of 733 b
11803: gap of 100 bp
25550: contig of 747 b
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23388: contig of 738 b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC094188
AC094188.2 GI:17940901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-2K16, 49 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 89536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pieces.
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Pred. No. 1
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1e-07;
ches 74; Indels 2;
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*** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 49 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15636537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
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Center clone name: CH230-2K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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4813: gap of unknown length
7442: contig of 2629 bp in length
7542: gap of unknown length
8970: contig of 1428 bp in length
9070: gap of unknown length
11618: contig of 2548 bp in length
11718: gap of unknown length
11718: gap of unknown length
14064: contig of 2346 bp in length
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             /organism="Rattus norvegicus"
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85795: gap of unknown 1
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Matches 72; Conserv
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|CCCTGCCCCAAATAGTGAAAAGCCACGTGAGT
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Homo sapiens junctophilin 3 (JPH3) gene, partial cds.
AF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potter.N.T., Ross.C.A. and Margolis.R.L. A repeat expansion in the gene encoding dasociated with Huntington disease-like Nat. Genet. 29 (4), 377-378 (2001) 21583737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 125020)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \label{eq:holmes} \begin{subarray}{ll} Holmes, S.E., & Ingersoll-Ashworth, R.G., & Ross, C.A. & and & Margollis, R.L. \\ Direct Submission & \end{subarray}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                             /product="junctophilin 3" complement(<36507. .>36887) /gene="JPH3"
               /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17466245"
/db_xref="GI:17466245"
/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS/translation="MSSGGRENEDDGSYCGGWEDGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAGNGKYEGTWSNGLQDGYGTETYSDG"
MGAKYEGTWSNGLQDGYGTETYSDG"
M32731 c 30696 g 28283 t 4254 others
                                                                                                                                                                                       /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                 complement(<36507. .36887)
/gene="JPH3"</pre>
                                                                                                                                                                                                                                                                                                                                                                                 complement(<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                               /note="JP3"
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Query Match Best Local Similarity

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Score Pred.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaagatggccggccgtggaccttcacccttctctgtggtttgctggcagccaccttgat 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSRSASSKCKGSRGMRRRSKRSSKYRKRGRGKKRSMTKSKGSKGKSKCWKRSGSMTSSCY 17747
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                                                                                                                        The cloning and sequencing of two cDNAs c of BSP30, a bovine member of the Parotid Unpublished
                                                                                                                                                                    Bovidae; Bovinae; Bos.

1 (bases 1 to 999)

Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
                                               Bag,
                                                                Submitted
                                                                               Direct Submission
                                                                                        2 (bases 1 to 999)
Haigh, B.J., Wilkins, R.J. and Wheeler, T.T.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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U79413.1 GI:1710366
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Bos taurus common salivary protein BSP30 mRNA,
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                                              itted (21-NOV-1996) Dairy Hamilton, New Zealand
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                Location/Qualifiers
1. .999
/organism="Bos taurus"
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GAAAGCCTGGATACAGA
                                                        AGACAGTTGGTGTCCTCTGTAGTGCAGCACGAGCTGTGCCCCACGAATCCGTGAACTCCTT
                                                                                  ggcccacccgcctggtcctcagtgactgtgccaccagccatgggagcctgcgcatccaa
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LDTECIKKLIGEPQVTTQQESEVHR"
247 c 255 g 230 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVQLWKLVLLCGLLAGTSESLLDIRGNDVLRRLISGLERGLGTF
DSTIEIIFQNLKTELESRCLNDVVEETQQTENSLEGLISRIFQVVNRLTGVRIRNVQV
PDITFEATSENSADVSIPITADVTVSLPLLGEIVKLDLNVDLQTSVSIETDAETGDSR
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/tissue_type="parotid
36..767
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/db_xref="GI:1710367"
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Pred. No. 0.026;
0; Mismatches 154;
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                                                          AUTHORS
TITLE
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AL356798
      Submitted (26-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk
On Sep 27, 2001 this sequence version replaced gi:14455883.
During sequence assembly data is compared from overlapping clone where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that together with a note of the overlapping clone name.
                                                                  Babbage, A.
Direct Submission
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                AL356798
Human DNA sequence
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variation annotation may not be found in the sequence submission
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AC08271 Homo sapi
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Autographa californica nuclear polyhedrosis virus HindIII K region
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT: This sequence is not the entire insert of clone RP11-467B11 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-467B11 is at 118068 in this sequence. The true left end of clone RP11-208F1 is at 29578 is sequence. The true right end of clone RP11-29B11 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr9
RPI1-467Bl1 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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VECTOR: pBACe3.6
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Friesen, P.D. and Miller, L.K.
Divergent transcription of early 35- and 94-kilodalton protein genes encoded by the HindIII K genome fragment of the baculovirus Autographa californica nuclear polyhedrosis virus
J. Virol. 61, 2264-2272 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unspliced messenger-active RNAs are transcribed from both 35- and 94-kd protein genes early (2 hours) after infection. Late in infection, abundant RNAs are transcribed from promoters located at least 2.5 kb upstream from the gene encoding the 35 kd protein. These transcripts completely overlap both the 35 and 94 kd polypeptide genes, but apparently lack protein-coding potential, suggesting that the transcripts may play a role in suppressing
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35 kDa protein; 94 kd protein.
35 kDa protein; 94 kd protein.
Autographa californica nuclear polyhedrosis virua (strain L-1) DNA,
passed in Spodoptera frigiperda IPLB-SF-21 cells.
Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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//TEANVLKINLLNEKPFSFERIVFYAINNTEQIDLSVASAFVUNSDCKIYRN
DEMVEWNILTKEENYD II.TTENRISKKDELLSFVTKFKFFYKTLYNADVLNEDNILNEUDKLKRL
RQRLESESIKOTHNSSSNMFDOIKKNEFFYLFYKTLYNADDDLSAYDYSNVENIRFPDC
IIANDSESIKOTHNSSSNMFDOIKKLASVNAETDDVVANDDDLSAYDYSNVENIRFPDC
IIANDSGVPAILLTHYNLFETTOGSLTKFKSRLEFFILMSONKEIKNSIEYCYNLESL
KQLIOHGTRLSPRSRRPFTGAIVPNEQEDEYNDYVAACTYFDAKKVAFRAGLMYYLEY
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MSVLDAVEMIANRAFECKDKFIINKLTNADALQDLKFLKVNHHGVVDBHVLKUTSINA
      VLYVKLHNVTSALNKNVILNTIK*
0 a 686 c 731 g 1208
upstream of HindIII site; 8
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LPSSFKNSEKVLYYNEASKNESMIYKALEFTTESSWGKSEKVNWKIFCNGFIYDKKSK
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complement(39. .2684)
complement(99. 4b mRNA (alt.)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERYLYFYHIIEDFDKYISVVDNTMRPAFVLEEGKTFYDSLLKQLQSVHFNGQEITFEK
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/note="early 35 kb mRNA (3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSRLDFNRILSLHKLYIECVKSLNKYPTLEEYQNYVYNQKHVKFNRIAIFPENILQNI
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			USA	20894,	a, MD	9) NCBI, Bethesda,	<u>a</u> <u>c</u>	JOURNAL
						Č	2 (bases 1 to 133894) Kuzio.J.	REFERENCE
-					•	586-605 (1994)	Virology 202 (2), 586 94303173 8030224	JOURNAL MEDLINE
	9, R.D.	and Possee,R.D. nuclear	and a nuc	Lopez-Ferber,M. apha californica	pez-F ha ca	Kuzio,J., e of Autogr	Ayres, M.D., Howard, S.C., The complete DNA sequence polyhedrosis virus	AUTHORS TITLE
			ie;	Baculoviridae;	Bacu	a nucreoporyneom s, no RNA stage;)	Viruses; dsDNA viruses, Nucleopolyhedrovirus. 1 (bases 1 to 133894)	REFERENCE
				· ·	oviru	a nucleopolyhedrovirus	Autographa californica	SOURCE
							122858 L22858.1 GI:510708	ACCESSION VERSION
	AR-2001 Le	L 29-MAR complete	ر م ۳۸	circul: clone	A Oviru	133894 bp DNA a nucleopolyhedrovirus	L22858 Autographa californica	LAZBOB/C LOCUS DEFINITION
								RESULT 4
,						41 114235	aagaaataacttttgagaaat 41 	Qy 21 8 Db 114255 <i>l</i>
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						to 133894) Possee,R. and Ayres,M.	1 (bases 1 to 133894) Bishop,D., Possee,R. and	REFERENCE AUTHORS
							unidentified unclassified.	ORGANISM
							unidentified.	KEYWORDS SOURCE
						r wosporzzo.	A48542 GI:2302312	ACCESSION VERSION
	07-MAR-1997		PAT	linear		133894 bp DNA	Ť Š	A48542/c A48542/c LOCUS
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VAQKTEELVKKQEFIERIVAIKDKQIEAKDLQVTRVMTDLNRMYTGFQETMQKKDEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1041. .2027)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKKDAQVTDLVAKVVDLSDRAVQYPADKRKHPVLCVTRDGTTFTAITGQKTYVENQKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="BRO; 37769 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "ITTODAAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acorf-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2750)
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Complement (5287. . . 6918)
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HDSKCVGEVMHLLIKSODVYKPPNCQKMKTVDKLCPFAGNCKGLNPICNY"
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Barbaria, J., Balbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Dowdhry, I., Christopoulos, C., Cleveland, C.D., Chen, Z., Chiu, D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Delgado, O., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homst, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Martin, R., Marti
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complement(7899. .8921)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (30-MAR-2001) Human Genome Sequencing Center, Der of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA on Mar 30, 2001 this sequence version replaced gi:13470106. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                        OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 142289)
                                              Contig length:
Phrap values in estimate:
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Direct Submission
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Direct Submission
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accatggaata(c) tatgcagcc
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gagactcgt(c) tcaaaaaaaaa
actccgtctc(a) aaaaaaaaaa
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cacgttgtgc(a)catgtaccct
acctaaattt(g)aaattgagca
agtgaaataa(a)ccagacacag
ttctgagttt(t)ctcagaaata
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acctggaaca(n)tcagcacctg

FEATURES Version: 1.01 qxfo. Location/Qualifiers /organism="Homo sapiens" .142289

Average error rate (BCM-Phrap estimate):

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FEATURES
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                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 were covered by at least assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SMISSPROT; Tr., TREMBL; WP:, WORMPEP; Information on the WORMPEP SHISSPROT CONTRACTOR OF THE SHIPPING CONTRACTOR OF T
                                                                                                                                                                                                             Group.
                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Mar 11, 2001 this sequence version replaced gi:12743783.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with many as described above.
                                                                                              http://www.chori.org/bacpac/home.htm
                                                                                                                          Pieter de Jong. For further details see
                                                                                                                                     RP11-9017 is from the library RPCI-11.1 constructed by the group of
                                                                             VECTOR: pBACe3.6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163283)
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                                                                                                                                                                                                     Further information can be found at
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1019. 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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/chromosome="12q"
/clone="RP11-543H12"
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3975..4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="CpG island"
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/chromosome="X"
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                                                                                                                                                                                          . 23594
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repeat:
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/note="MER5A repeat: matches 4.
24307. .24871
                            /note="MLT1E repeat: matches 1. 25135. .25364
                                                                                                                         /note="MIR repeat: matches 48. .256 of consensus"
                                                                                                                                                                    /note="L2 repeat: matches 2699.
                                                                                                                                                                                                           'note="MLT1J repeat: matches 1.
                                                                                                                                                                                                                                                  /note="tRNA-Gly-GGC repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                  /note="L1P3_repeat: matches 1. .4059 of consensus"
                                                                                                                                                                                                                                                                                                                                                                   /note="L1P repeat: matches 4285. .4621 of consensus"
15572. .19938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=".117416 repeat: matches 5383. .6157 of consensus"
                                                                                                                                                                                                                                                                                                'note="LlP repeat: matches 5155.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1P repeat: matches 4046. .4299 of consensus"
14958. .15248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13805. 13029
/note-"AluJo repeat: matches 86. .311 of consensus"
13148. 13910
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6719. .7019
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10518. .10971
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/note="AluSg repeat: matches 1.
9794. .9919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11.1"
1004. .1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="MIR repeat: matches 102.
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                                                                                                                                                                                                                                                                                                                                                                                                      "LIP repeat: matches 4603, .4893 of .15575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L1PA7 repeat: matches 5347. .6143 of consensus"
.14957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L2 repeat: matches 902. .1813 of consensus"
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matches 109. .319 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .297 of consensus
                                           .553 of consensus"
                                                                                  .153 of consensus
                                                                                                                                                                  .2750 of consensus
                                                                                                                                                                                                           .165 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2179 of
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repeat_region
                                      /note="Alux repeat: matches 1. .308
51249. .51339
                                                                         /note="L1MD1 repeat: 50940. .51248
                                                                                                                                                                                                                            /note="FLAM_A repeat: matches 4. .133 of consensus" 47030. .47196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Tigger3(Golem) repeat: matches 1. 31455...34275
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25872. .25911
                                                                                                                                                                                                                                                                                                   note="McR53 repeat: matches 1. .187 of consensus" 45981. .46564
                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 47.
14468. .44799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1M4c repeat: matches 789. .1908 of consensus"
42508. .42799
**RiuJb repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1PA5 repeat: matches 2840. .3298 of consensus'
35039. .35092
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29055. .30453
                                                                                                                                 /note="L1PA4 repeat:
                                                                                                                                                                    note="L1MD1 repeat: matches 5096.
                                                                                                                                                                                                       'note="MIR repeat: matches 10. .164 of consensus"
                                                                                                                                                                                                                                                                              'note="L1MB6 repeat: matches 5573. .6172 of consensus"
                                                                                                                                                                                                                                                                                                                                                        note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 3. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="53 copies 2 mer tt 65% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"L1M4 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="L1M4 repeat: matches 2135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note "LIPA5 repeat: matches 1. .2855 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSc repeat: matches 17. .309 of consensus"
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95. .35842
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                   repeat: matches 4549. .4641 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches
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                                                                                            matches 4641.
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                                                                                                                               .6146 of consensus
                                                                                                                                                                    .6213 of consensus
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                                                        of consensus*
                                                                                            .5093 of
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6 (bases 1
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Waterston,R.H.
Direct Submission
Submitted (28 SEP-1999) Genome
University School of Medicine,
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Submitted (O8-SEP-1999) Genome Sequencing Center, Washington University..... School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
Submitted (31-JUL-1999) Genome
University School of Medicine,
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                                                                                                       Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 8, 1999 this sequence version replaced gi:5732142.
                                                                                                                                                                        Waterston, R.
Direct Submission
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5 (bases
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                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu/gsc
Center project name: H_NH0575G01
                       Contact: sapiens@watson.wustl.edu
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53242. .53938
/note="LIRB repeat: matches 31. .691 of consensus"
53939. .54218
/note="LIPB3 repeat: matches 5867. .6143 of consensus"
54828. "55070
/note="MIR repeat: matches 2. .262 of consensus"
56554. .57365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov/ or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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                                                                                                                                                                                                                   complement(4103. .>50924)

//gene="WUGSC:H_NH0575001.1"

complement(join(<4103. .4261,26454. .26553,30330. .30380,32481. .32550,50795. .>50924))

//gene="WUGSC:H_NH0575601.1"

//note="match to JH0565 (PID:g87003); H_NH0575601.1"
                                  MLETLSDDDFYNYASFNSNAQDYSCFQHLYQANYRNKKYLKDAYNNITAKGITDYKKG
                                                          /translation="TivlnelnwTsALDEVFKKNREEDPSLLWQVFGSATGLARYYPA
SPWVDNSRTPNKIDLYDVRRRPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSE
                                                                                                                                                                  precursor"
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                                                                                                                /protein_id="AAF19234.1"
/db_xref="GI:6624059"
                                                                                                                                                                           /product="match to calcium channel alpha-2b chain
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2332. .2753
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3223. .3517
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/clone="RP11-575G1"
/clone_lib="RPCI-11"
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/db_xref="taxon:9606"
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/note="match to EST N85205 (NID:g1260830)"
26648. .26675
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25734. .26165
                                                               note="match to EST AI434840 (NID:g4298992) til3a04.x1"
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20431. .20
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18853
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19017. .19295
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8711. .9067
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/note="match to EST N85205 (NID:g1260830)"

4212. .4256

/note="match to EST AI434840 (NID:g4298992
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11733. .11927
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                                                                                                                                                                                                                                                                                                                                                 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/Cgi-bin/sp.cg1). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-NOV-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) Plant 29, 2000 this sequence version replaced gi:6451951. On Jun 29, 2000 this sequence version replaced Address for correspondence: kaos@kazusa.or.jp Roor correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/Kaos/cg1-bin/agd_graph.cg1?c=K17E7 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,231,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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20; Conserv
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                                                                                                                                                                                                                                                         r because we remove overlaps between neighboring submissions. clone is T26Gl2 and the 3' clone is T20F20.

Location/Qualifiers
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27603. .28308
                 polyprotein
gene_id:K17E7.1"
                                          /note="contains similarity to retroelement pol
                                                                                       /clone
                                                                                                                  /clone="K17E7"
                                                                                                                                         /chromosome="3"
                                                                                                                                                                  /db_xref="taxon:3702"
                                                                                                                                                                                      /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                            lib="Mitsui TAC"
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7.3
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/evidence-not_experimental
join(25276. .25546,26136. .26343,26806. .27063,27478.
27647. .27820,28233. .28440,29579. .29743)
/note-"gene_id:K17E7.8
unknown protein"
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join(12471. .12477,12881. .13057,13190. .13277,13381. .13486)
/note="gene_id_K17E7.5"
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complement(join(9810.
/note="emb|CAB88116.1
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DQKSQHVGEAYMKMLEERMSEIDKDGPQISGNSSQHSTHRMLSIDEKNEIFFKCTLTD
GKGNPFGLGSLVETLNKRRRTESYASSSSTVAQLQEQLQLKMSEQAEQNAKCDEEHRQ
LRLVLFPRRDLFVGEEKPSLICDVFAGNHDFHAVSSQLSHKFVREIFVTKFATEYRLG
PVPSQSSRNSVAI"
                                                                                                                                                                            CRRDLFVGEEEVCRRDLFVGKFEVCGENNSSSNLSFIRENNSSANLKIYSSAKKRFVR
EIYSSAKKRFVEEIYSSANLRFVGENNSSANLSFIGQNNLSANLSFIRENNSSANLSS
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EAEALAILAALTQARSLGFSFIPSSANCEADLLAKHALCAFESNSVPRHVEKQKSYSG
VKRSKQSGFTHHPSKSSSANFIL"
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NLVVedseidedcsiwgkpkkkgssifrkpkkkeetttiilQenlQfatpilvpkwlQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/protein_id="BAB02992.1"
/db_xref="GI:13477079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to unknown protein"
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                                                        SANLSRISYRRKCVATYGGTQFPQSPRKFATFLRGIMTSTQFPRNCLANLRGKYLSQS
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/translation-"MTYTQFPRNCLANVRGKYSSQNLRRNSELVMFPRRDLFVGEEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene_id:K17E7.7"
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complement(20744, 29799)
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                                                                                        HWLANLEIYSSAKKRFVGEIYSSTKKRFVGEIYSSANLRFVGENNSSANLSFIGENNS
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17203. .187
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join(8339. .8392,8478. .8714,8838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to TNP2-like transposon
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Similarity
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similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                               similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTPTCCVSLSAFYNETIVPCPTCSCGCONSSOAGTCVDCDSPKIASVVPALGKNNLEP
LLQCTQHMCPIRVHWHYKTSYKEYWRYKVAITNENYNMNYSQWNLVVQHENEDNLTKL
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                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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gene_id:K17E7.9"
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  6.3%; 5c.
100.0%; Pr
                                     Pred. No.
          Mismatches
                                                           DB 8;
                                   7.2;
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     0;
  Gaps
0;
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                        TITLE
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        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                      Center code: BCM
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CDS

Matches Best Local

Project Information

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RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, M., Bryant, N.P., Buhay, C., Burch, J., Burch, J., Burch, J., Brown, J., Brown, M., Bryant, N.P., Buhay, C., Carter, M., Gavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elscotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Gouvara, W., Gunrathe, P., Hale, S., Herlandez, O., Hodyson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Youdah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kurshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Maritin, R., Martin, R., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Culles, M., Rei, J., Novem, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwon, G., Oragunye, N., Nickenson, E., Nwokenkwo, S., Suson, I., Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, K., Tang, H., Surdal, R., Wall, R., Wang, S., Waren, N., Pickens, R., Primus, E., Pu, L., Stonals, R., Stonals, R., Vang, S., Wall, R., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaattttgaaaatagattgt
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                                                    Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                             Baylor Plaza, Houston,
                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                              Worley, K.C.
                                                                                                                                                                                                                                                                                                                            Worley, K., Wu, C., Wu, Y., Weinstock, G. and Gibbs, R. Direct Submission
                                                                                                                                                                                                                                                                                          Unpublished
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Rattus norvegicus clone CH230-127D2,
***,52 unordered pieces.
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                                                                                                                                                                                                                                                            (bases 1 to 87966)
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   Center: Baylor College
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                                         Genome Center
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of Medicine
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2, *** SEQUENCING
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IN PROGRESS
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Assembly program: Phrap; version 0.990329First call findPhrapList
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NOTE: This is a 'working draft' sequence. It currently
consists of 52 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 64078 bases at least Q40 Consensus quality: 70281 bases at least Q30 Consensus quality: 75712 bases tat least Q20 Estimated insert size: 54379; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.5x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH230-127D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8539: gap of 11712: contig 11812: gap of 114902: contig 15002: gap of 16825: gap of 16825: gap of 18687: contig 18
          50789:
50889:
52357:
52457:
53677:
53777:
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46053:
47550:
47650:
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39324:
39424:
40701:
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36482:
36582:
37738:
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3455: gap of
6405: contig
6505: gap of
8439: contig
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                     gap of contig                                                                                                                                                                                                                                                           gap of contig gap of contig gap of contig gap of contig
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of 1934 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and geneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/rdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC clone F21N10 is from Arabidopsis thaliana chromosome The orientation of the sequence is from SP6 to T7 end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-SEP-2000) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, cdtcwn@tigr.org On Sep 12, 2000 this sequence version replaced gi:7709919. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (26-MAR-2000) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 98017) Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F21N10 genomic sequence
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                                                                                                                                9525. .9634
/TPt_family-"ARNOLD1|ARNOLD1
         10984. .11112
/rpt_family="ARNOLD3|ARNOLD3
ARNOLD3."
                                                                                                                                                                                                                                                                                                                           9506.
                                                                                                                                                                                                                                                                                                                                                                               8803. .8913
/rpt_family="ARNOLD2|ARNOLD2 Autonomous DNA-transposon ARNOLD2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8803. .8913
/rpt_family="ARNOLD1|ARNOLD1 Autonomous
ARNOLD1."
                                                                          /rpt_family="ARNOLD2|ARNOLD2
ARNOLD2."
                                                                                                                                                                                                             /rpt_family="ARNOLD4|ARNOLD4 Autonomous DNA-transposon
ARNOLD4."
                                                                                                                                                                                                                                                                                  ARNOLD3
                                                                                                                                                                                                                                                                                                                                         /rpt_family="ARNOLDY2|ARNOLDY2 Non-autonomous DNA
transposon ARNOLDY2 - a consensus sequence."
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ARNOLD3."
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ARNOLD1."
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ARNOLD4."
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/rpt_family="ATCOPIA151|ATCOPIA151 Internal region of ATCOPIA15 copia-like LTR-retrotransposon."
                                                                                                                                                                                                                                                                                         'rpt_family="ARNOLD3|ARNOLD3 Autonomous
ARNOLD3 "
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ARNOLD1."
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ARNOLD4."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="ATCOPIA11|ATCOPIA11 Internal region of
ATCOPIA1 LTR-retrotransposon."
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ARNOLD2."
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3037. 3795
/rpt_family="ATCOPIA151|ATCOPIA15I Internal region of ATCOPIA15 copia-like LTR-retrotransposon."
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ARNOLD3."
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                                                     KEYWORDS
                                                                                        ACCESSION
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                                                                                                                                                                                                                                                                                                                      Local
                                                   AC096828
AC096828.2 GI:17972957
HTG; HTGS_PHASE1.
                                                                                                 AC096828 109981 bp DNA linear Rattus norvegicus clone CH230-91G16, *** SEQUENCING ***, 59 unordered pieces.
                                                                                                                                                                                                                                                                                                     20;
                Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                   6.3%; ilarity 100.0%; Conservative
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/rpt_family="centromeric repeat T5H22 31150 to
16107_ .16191
                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="centromeric repeat T5H22 31150 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="ARNOLD2|ARNOLD2 Autonomous DNA-transposor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="ARNOLD4|ARNOLD4 Autonomous DNA-transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="ARNOLD3|ARNOLD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="ARNOLD4|ARNOLD4 Autonomous DNA-transposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="ATREP5|ATREP5 An AT-rich repetitive sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _family="ARNOLD1|ARNOLD1 Autonomous DNA-transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="ARNOLD2|ARNOLD2 Autonomous DNA-transposor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="ARNOLD1|ARNOLD1 Autonomous DNA-transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family="ARNOLD3|ARNOLD3 Autonomous DNA-transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="ARNOLD3|ARNOLD3 Autonomous DNA-transposon
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Pred. No.
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7.1;
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COMMENT

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Davy-Carroll, D. Dederich, D. A., Delandy, K. R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hemandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Ulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morris, S., Moser, M., Michell, T., Mohabbat, K., Mguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Ouiles, M., Ren, Y., Rives, M., Rojab, A., Rojubokan, I., Rolfe, M., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tangrisa, K., Wall, R., Wang, S., Warfen, R., Washington, C., Visson, R., Wall, R., Washington, C., Visson, R., Wall, R., Wang, S., Warren, R., Washington, C., Visson, R., Wall, R., Washington, C., Visson, R., Wall, R., Washington, C., Wall, R., Wang, S., Warren, R., Washington, C., Visson, R., Wall, R., Wang, S., Warren, R., Washington, C., Visson, R., Wall, R., Wang, S., Warren, R., Washington, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15799472.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 59 contigs. The true order of the pieces
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Submitted (09-MAY-2001) Department of Genetics, Washington
Submitted (109-MAY-2001) Department of Genetics, Wissouri 63108,
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Nov 8, 2000 this sequence version replaced gi:9838078.
                                                                                                                                                                                                                                                                                                                                                                                            SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                      The sequence RP11-123E16 contains a dinucleotide (GA) repeat from base position 3114 to 3320. There is single subclone coverage and the fidelity of sequence cannot be guaranteed. The region corresponds to restriction digest information: BamhI band size 6715 real and 6686 in silico; and HindIII band size 3806 real and
                                                                                                                                                                                                                                  The clone sequenced to the left is RPI1-422A6, 200 bp overlap; the clone sequenced to the right is RPI1-120J4. Actual start of this clone is at base position 84248 of RPI1-422A6; actual end is at base position 111159 of RPI1-123E16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Direct Submission
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University School of Medicine, 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                             (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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E 1 (bases 1 to 114927)

E 1 (bases 1)

Muzny,D,M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Deny,Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
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Local Similarity 100.0%; Pred. No.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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18324. .19402
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Miner, Z., Mitchell, T., Mohabbat, K., Muyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Petry, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wailiams, G., Williamsson, A., Waeczyk, R., Wooden, S., Waerien, K., G. and Gibbs, R.
Worley, K.C.
                                                                                                                                                                       Unpublished
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COMMENT

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

TITLE

Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: GNKB
Center clone name: CH230-131J4
Center clone name: Summary Statistics

findPhrapList Assembly program: Phrap; version 0.990329First call to

Consensus quality: 92543 bases at least Q40 Consensus quality: 99732 bases at least Q30 Consensus quality: 104520 bases at least Q20 Estimated insert size: 74569; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 60 contigs. The true order of the pieces is not known and their order in this sequence record is as soon as it is available and the accession number will be preserved. 4014 4114 8453 8553 11387 8452: 8552: 11386: 11486: 4113: gap of 8452: contig 4013: contig gap of contig unknown of 2834 of 4013 bp in length unknown length of 4339 4 bp in length
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14815: 14915: 18585:

gap of contig gap of contig

unknown of 3670

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76033:
76123:
78122:
78222:
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Man, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Myokenkwo, S., Oguh, M., Okwnon, G., Oragunye, N., Oviedo, R., Parce, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., J., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Stanley, H., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Walliams, S., Warde, Moore, S., Warren, R., Washington, C., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Warren, R., Washington, C., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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NOTE: This is a "working draft" sequence. It currently consists of 71 contlys. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-100419 The true left end of clone RP11-500011 is at 24031 in this sequence. This
                                                                                                                                                                                                                Submitted (09-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 21, 2000 this sequence version replaced gi:6983194.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission conly a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSJ100419 117757 bp DNA linear PRI Human DNA sequence from clone RP5-100419 on chromosome ESTs, STSs and GSSs, complete sequence.
left end of clone RPI1-500011 is at 24031 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="26
6133. .697
                                                                                                                                                                                                                                                                                                                                                                 /note="L2 re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5841. .6068
/note="MER46A repeat: matches 6078. .6129
                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 8. 9122. 9174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6133. .6977
/note="LLPA3 repeat: matches 5286.6978. .7495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2913. 2975
/note="MER3 repeat: matches 145. .207 of consensus"
4751. .5056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="THE1B repeat: matches 1. 2913. .2975
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265. .:
                                                                                                                                                                                                                                                                                                                                                       8686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="LTR16C repeat: matches 272. .354 of consensus" 914. .1290
  /note="match: GSS: Em:AQ549175"
18512. .18622
                                                                                                                                                        /note="MIR repeat: matches 23. .236 of consensus" 15726. .16149
                                                                                                                                                                                                                                                                                                         complement(10194.
                                                                                                                                                                                                                                                                                                               /note="11 copies 2 mer at 100% conserved'
complement(10194. .11028)
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/note="LTR16C repeat: matches
                                        complement(18234. .18628)
                                                                                                                                                                                                                                                                           /note="match: GSS: Em:AQ738844"
10451. .10635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8496.
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/note="Aluy repeat: matches 2. .296 of consensus"
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/clone_lib="RPCI-5"
                                                        /note="AluJb repeat: matches 1.
                                                                                                /note="MLT1A1 repeat: matches 1. .363 of consensus"
                                                                                                                                      /note="L1MB3 repeat: matches 5050.
                                                                                                                                                                                                                                    11814.
                                                                                                                                                                                                                                                     /note="MER5A repeat: matches 2.
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/note="L1PA3 repeat: matches 4747.
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                                                                              .18145
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                                                                                                                                                                                                                                12073
                                                                                                                                                                                                12796
                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 2688. .2735 of consensus"
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                                                                                                                                                                                                                repeat:
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                                                                                                                                                                                                                  matches 2468.
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                                                                                                                                                                                                                                                                                                                                                                                                             .241 of consensus"
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repeat: matches 6.

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                         substitution"
/replace="atg"
30483. .30544
                                                                          acg in this entry
                                                                                                                                           /note="clone RP11-500011
cat in this entry
substitution"
/note="31 copies 2 mer tt 72% conserved"
                                                                                                              /replace="cgt"
29849. .29851
                                                                                          /note="clone RP11-500011
                                                                                                                                                                                                                                    substitution"
                                                                                                                                                                                                                                                                                                                                                                                  /note="L2 repeat: matches 2623. .2736 of consensus" 28412. .28608
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/note="MER5A repeat: matches 91. .171 of consensus"
20014. .20350
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubstitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="L1MC4 repeat: matches 6626.
17203. .27350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="24 copies 2 mer ga 72% conserved"
23918. .23978
/note="MIR repeat: matches 28. .90 of consensus"
24098. .24217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="10 copies 8 mer aaaggagg 67% conserved" 7479. .27535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER5B repeat: matches 66. .178 of consensus"
25225. .25542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="16 copies 4 mer tcct 68% conserved" 24365. .24469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-*15
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'note="L1ME3A repeat: matches 6015. .6157 of consensus"

23151. .23198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC4 repeat: matches 7288. .7768 of consensus"
22623. .22714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="8 copies 4 mer caca 93% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20014. .20350
/note="THEIB repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20477. .20532 Thorte="7 copies 8 mer cacacac 80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 39. .131 of consensus"
                                                                                                                                                                                                                                                                                                                               e="Charlie2 repeat: matches 1. .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                     :e="MIR repeat: matches 40. .250 of consensus"
14. .29255
                                                                                                                                                                                                                                                   in this entry
                                                                                                                                                                                                                                                                                                e="Charlie2 repeat: matches 233.
                                                                                                                                                                                                                lace="agc"
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8. .27557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="clone RP11-500011
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e="21 copies 2 mer ac 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                          ace="taa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ="19 copies 3 mer gag 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lace="gcc"
                                                                                                                                                                                                                                                                   ="clone RP11-500011
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.24215
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              47 aaatgaaatcágtttctcca 66
                                                  h 6.3%; Score 20; DB Similarity 100.0%; Pred. No. 7; 20; Conservative 0; Mismatches
                                                                                                                   /replace="cca"
33016. 33018
/note="clone RP11-500011
cct in this entry
substitution"
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/note="clone RP11-500011
aac in this entry
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0668. .30795
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Search completed: September 16, 2002, 06:31:07 Job time: 12345 sec

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Perfect score:
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380 a 503 c 429 g 367 t 1 others	/organism="Homo sapiens" /db_xref="taxon:9606"	11680	Location/Qualifiers	diaDexus, Inc. (US)	Patent: WO 0161055-A 1 23-AUG-2001;	lung cancer via lung cancer specific genes	Methods for diagnosing, monitoring, staging, imaging and treating	Chen, S.Y., Sun, Y. and Macina, R.A.	1 (bases 1 to 1680)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX224643.1 GI:15554772	AX224643	Sequence 1 from Patent WO0161055.	AX224643 1680 bp DNA linear PAT 10-SEP-2001		

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Mammalla; Butheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 2036)

Chen,S.Y., Sun,Y. and Macina,R.A.

Methods for diagnosing, monitoring, staging, imaging

lung cancer via lung cancer specific genes

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Query Match
Best Local Similarity
Matches 1627; Conser

Conservative

86.7%; 99.9%;

Score 1457; D Pred. No. 0; 0; Mismatches

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            ACATCCCGTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGTGTGC
                                                        acatocogttcagoctcatogtgagtcaggacgtggtgaaagctgcagtggctgctgtgc
                                                                      GAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCCACCCTGGACA
                                                                          gaaaggtgaccaagtggttcaataactctgcagcttccctgacaatgcccaccctggaca
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
1 (bases 1 to 1684)
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R. M.
                      Web site:
Contact:
                                                                                      NIH-MGC Project URL: http://m
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
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                                                                                                                                                  Direct Submission
Submitted (25-MAY-2001) Nat.
Gene Collection (MGC), Cance
Institute, 31 Center Drive,
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BC008429
BC008429.1 GI:14250057
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        http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford
M., Schmutz, J., Grimwood, J., Rodr:
                                                                                                                                                                                                                                                                                                             1684 :
s, Similar to DNA :
f Technology 19, c
                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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                                                                                                                                                 ) National Institutes of He
Cancer Genomics Office, Na
rive, Room 11A03, Bethesda,
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      Rodriquez,
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National Cancer
da, MD 20892-2590,
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cccaagccaccatccgcatggacaccagtgcaagtggccccacccgcctggtcctcagtg
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
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KCHNATSILQQLPLLSAMRERAGGIPVLGSLVNTVLKHVIWLKVITANILQLQVKPS
ANDQELLVKIPLDMVAGFNTPLVKTIVBFHMTTEAQATIRMDTSASGETRLVLSDCAT
SHGSLRTQLLKKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIBASENGVADLLQL
VKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQKVTKWFNNSAASLTMPTLD
UIPFSLLVSQDVVKAAVAAULSPEEPMVLLDSVLPESAHRLKSSIGLINEKAADKLGS
TQIVKILTQDTPEFFIDQGHAKVAQLIVLEVPFSSEALRPLFTLGIEASSEAQFYTKG
DQLILMLNNISSDRIQLMNSGIGWFQDDVLKNIITEIIHSILLPNQNGKLRSGVPVSL
VKALGFEAAESSLSKDALVLTPASLWKPTSPVSQ"

493 c 414 g 358 t
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Institute of Technology 19"
/protein id="AAH08429 1"
/db_xref="GI:14250058"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:14597 IMAGE:4291561"
/tissue_type="Skeletal Muscle"
/clone_lib="NIH_MGC_81"
/lab_host="DH10B"
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          CATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCC
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                                                                                                              GGGCAGCCTGGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAGDWTFTLLCGLLAATLIQATLSPTAVLLIGEKVIKEKLTQEL KDHNATSILQLDLLSAMREKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLCVKPS ANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTTEAQAATIRMDTSASGETRLVLSDCAT SHGSLRTQLLKKISELVNALAKVYMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQL VKGRCSALSPTESETTELASREGKVXKWFUNSAASLIMPTLDNIPFSLIVSQDVVKAA VAAVLSPEEEFMVLLDSVVNLSTRQRIGPPRPHHRNFLNTGCP"

333 c 261 g 211 t
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/db_xref="taxon:9606"
79. 1035
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/db_xref="GI:17382959"
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99.9%;
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Pred. No. 1e-303;
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Best Local Similarity
Matches 405; Conserv
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                                      AGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCTGGTCA
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Sequence
AX301906
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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314 c 237 g 195 t
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                                                                                                                                                                                                                                                                                                              /protein_id="CAD13089.1"
/db_xref="GI:17382957"
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/db_xref="taxon:9606"
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from Patent WO0174851.
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                                                                                                                                                                                                                                                                                                                                                                                 where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: PMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 wapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cttccttcaatggcatgtatgcagacctcctgcagctggtgaagg 783
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                                                                             http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RP5-1187J4 The true
left end of clone RP11-37D19 is at 62286 in this sequence. The
left end of clone RP11-37D19 is at 100 in this sequence. This
sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP5-1187J4 is from
the laborate of the confirmed by restriction digest. RP5-1187J4 is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 14, 2001 this sequence version replaced gi:6982468 gi:9213549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human DNA sequence from clone RP5-1187J4 on chromosome 20q11.1-11.23 Contains ESTs, STSs, GSSs and two CpG islands. Contains the gene for novel protein similar to mouse von Ebner salivary gland protein, the gene for a novel protein similar to rat RYF3, the LOC51654 gene for a novel protein (CGI-05) similar to rat CDK5 activator-binding protein and the SNTA1 gene for alpha syntrophin (dystrophin-associated protein A1, 59kD, acidic
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AL355392.7 GI:10
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        http://www.chori.org/bacpac/home.htm
                                                      the library RPCI-5 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                     further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGI-05; CpG island; RYF3; SNT1; SNTA1; syntrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence assembly data is compared from overlapping clones
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/clone="RP5-1187J4"
/clone_lib="RPCI-5"
1535. .1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WKPSSPVSQ" 3817. .3919
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1757. .18
                                                                                                                            complement(6761. .7253)

/note-"match: GSS: Em:AQ149447"

join(7182. .7295,8242. .8295,8799. .8957,9841. .9908,

10729. .10774,11885. .11948,12794. .12870,15591. .15650)

/gene-"dJ1187J4.1"
                                                                                                                                                                                                                                                                                                                                                          match: ESTs: Em:AI924632 Em:AW363590 Em:AW384404 Em:AW449208 Em:AW167650 Em:AW381927 Em:AW167610 Em:AW677643 Em:AH7176323 Em:AI024451 Em:AD5555 Em Em:AW176327 Em:AW176325 Em:AI909965 Em:AI909964 Em:AA428580 Em:AW384465"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /9ene="dJT18JJ4.1"
/9ene="dJT18JJ4.1"
join(<3408. 3471,5782. .5867,7116. .7295,8242. .829;
8799. .8957,9841. .9908,10729. .10774,11885. .11948,
12794. .12870,15591. .15650)
/evidence=not_experimental
/product="dJ1187J4.1.2 (novel
Ebner salivary gland protein,
/protein_id="CAC15880.1"
                                                                                                                                                                                                                           complement(6761. .7253)
/note="most"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: STS: 3917. .4143 /gene="dJ1187J4.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: STS: Em:G10242"
complement(join(3917. .4006,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Tandem repeat. weak data"
join(3408. .3471,5782. .5867,7116. .7295,8242. .8295,
8799. .8957,9841. .9908,10729. .10774,11885. .11948,
12794. .12870,15591. .15761)
                                                                                                                                                                                                                                                                                                      /product="dJ1187J4.1.2 (novel protein Ebner salivary gland protein, isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALGFEAAESSLTKDALVLTPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FMYLLDSVLPESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQ
LIVLEVFPSSEALRPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebner salivary gland protein,
/protein_id="CAC34050.1"
/db_xref="GI:13274680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: ESTs: Em:BE933124 Em:BE061388"
/product="dJ1187J4.1.1 (novel protein similar to
Ebner salivary gland protein, isoform 1.)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4662. 4691
/note="15 copies 2 mer tt 86% conserved"
join(5758. 5867,7116. .7295,8242. .8295,8799. .8957,
9841. .9908,10729. .10774,11885. .11948,12794. .12870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="LCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDT
IQLYLGAKLLDSQGKVTKWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEE
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/product="dJ1187J4.1.1 (novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15591. .15761)
/gene="dJ1187J4.1"
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                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: cDNAs: Em:U46068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Continues in Em:AL121901 as bA49G10.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                               protein similar to mouse von isoform 2.)"
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                                                                                                                                                                                                                                                                                                           similar to 2.)"
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                                  unatch: STS: E
complement(39991. .4.
/note="match: GSS: E-
complement"
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complement(22577...2
/note="match: GSS: El
22977...23573
complement(40002.
/note="match: GSS:
                                                                                                                                                                                                                                   complement(39950. . /note="match: GSS:
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complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complement/complemen
                                                                                                                                               complement (39964.
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/note="match: GSS: Em:AL2"
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complement(39266. .
/note="match: GSS:
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complement(39112.
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complement(37780
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/note="match: GSS:
complement(20698.
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39747. .40042
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/note="match:
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SILLPNONGKLRSGVFVSLVKALGFEAAESSLTKDALVLTPASLWKPSSPVSQ"
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15761
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15754
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/note="match: GSS: Em:AQ373301"
11775. .12108
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14836. .14871
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11766. .12192
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11768. .12108
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.4322. .14833
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.18004)
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.11769)
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                                                        Em: AQ596761"
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Best Local Similarity
Matches 181; Conserv
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requests: clonerequest(sanger.ac.uk)
On Jun 5, 2000 this sequence version replaced gi:8017404.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROY; Tr: , TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
IMPORRANT: This sequence is not the entire insert of clone RP1-49G10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP5-1187J4 is at 161494 in this sequence. The true right end of clone RP5-1187J4 is at 161494 in this sequence. The sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from clone RP11-49G10 on chromosome 20 Contains a gene similar to bovine salivary protein BSP30, the LOC51297 gene for LUNX protein, 5' end of a gene encoding a protein similar to murine von ebner minor salivary gland protein, a novel gene, a pseudogene similar to STAT-induced STAT inhibitor-2, a pseudogene similar to ribosomal protein L12, a putative novel transcript, ESTS, GSSs and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL121901.20 GI:8249854
HTG; BSP30; CpG island; LOC51297; LUNX; RPL12; STAT-inhibitor.
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Mammalia;
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ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 161593)
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Pred. No. 9.9e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //www.chori.org/bacpac/home.htm
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/note="LIPB3 repeat: matches 5941. .6084
5140. .5183
                                                                                 23950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Tandem repeat. Forced join. Approximately 500
missing according to restriction digest."
16219. .16387
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/note="LIPA2 repeat: matches 5986.
/omnlement(6104. .6463)
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/note="match: GSS: Em:AQ607627"
                                                                                                                                                                 complement(21172. .21428)
/note="match: GSS: Em:AQ:
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                                                                                                                  complement(23637
                                                                                                                                               complement(23473.
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18328. .18828
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/note="22 copies 2 mer tt 75% conserved"
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/note="match:
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complement(14766. .15061)
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/clone_lib="RPCI-11.1"
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/db_xref="taxon:9606"
                                                                                                 'note="match: GSS:
                                                                                                                                 /note="match: GSS:
                                                                                                                                                                                              /note="41 copies 2 mer ag 75% conserved"
                                                                                                                                                                                                                                    note="match: GSS: Em:AZ055779 Em:AZ084220"
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               /note="match: 54767. .55668
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//db_xref="GI:9801234"
//translation="MLQLWKLVLLGGVLTGTSESLLDNLGNDLSNVVDKLEPVLHEGL
ETVDNTLKGILEKLKVDLGVLQKSSAWQLAKQKAQEAEKLLNNVISKLLPTNTDIFGL
KISNSLLLDVKAEPIDGGKGLMLSFPVTANVTVAGPIIQIINLKASLDLLTAVTIET
DPQTHQPVAVLGECASDPTSISLSLLDKHSQIINKFVNSVINTLKSTVSSLLQKEICP
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join(35535 .35585,36507 .36678,40308 .40452,41455 .4
42783 .42935,45523 .45604,46980 .47043,47896 .47973,
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/note="3 copies 60 mer 73% conserved"
                                                /note="match: 54041. .54149
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/product="bA49G10.1 (similar
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/gene="bA49G10.2"
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Sequence 68 from Patent WO0174851.
AX301961
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel proteins and nucleic acids encoding same Patent: WO 0174851-A 68 11-OCT-2001; Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Majumder, K., Spaderna, S.K., Taupier, R.J., Padigaru, M., Burgess, C.E., Shimkets, R.A., Spytek, K.A., Liu, X., Patt
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/db_xref="taxon:32630"
/note="Ag719 Probe Primer Sequence"
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Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,
Tangy,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N.,
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
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Consensus quality: 73144 bases at least Q40 Consensus quality: 80017 bases at least Q30 Consensus quality: 85368 bases at least Q20 Consensus quality: 85368 bases at least Q20 Estimated insert size: 69357; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                 Center clone name: CH230-2K16
------ Summary Statistics
Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ project Information
Center project name: CAEB
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Lusis, J., Xia, Y.-R. and Ya
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                          Submitted (21-SEP-1999) to the DDBJ/EMBL/GenBank databases. Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mailimika@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp, Tel:81-3-5214-8491, Fax:81-3-5214-8470)

This sequence is conducted by Japanese Foundation for Cancer Research as a JST sequencing Team.

Principal Investigator: Yusuke Nakamura Ph.D Phone: +81-3-5449-5372, Fax:+81-3-5449-5433, Yusuke@hgc.ims.u-tokyo.ac.jp
                                                                                                                                                                                5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
                                                                                                                                                                                                                                                                   Japan Science and Technology Corporation (JST)
                                                                                                                                                                                                                                                                                                    project of JST
                                                                                                                                                                                                                                                                                                          yusuke@hgc.ims.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura,Y., Isomura,M., Daigo,Y., Tamari,M. and Ishikawa,S. DNA sequence analysis of a 1.2-Mb region on chromosome 3p21.3 Published Only in DataBase (1999) In press 2 (bases 1 to 200000)
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                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/note="stSG9202; The location is between
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TAPIALSPGALEFGLLSPAIQDSNILLNLKAKLLDSQARVTNWFNNSATSLMSTTPDG
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/protein_id="AAA87581.2"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Expression of neurturin, artemin, persephin and
GFRa-2 and GFRa-3 in the mature rat cochiea
unpublished
Submitted (13-SEP-1999) Kresge Hearing Research Institute, University of Michigan, 9301E MSRB III, 1150 West Medical
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Stover,T., Gong,T.-W., Cho,Y., Altschuler,R.A. and Lomax,M.I.
Direct Submission
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                 RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blinage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Bieva, M., Bryant, N.P., Bouck, J., Bowie, S., Bieva, M., Bryant, N.P., Bouck, J., Bowie, S., Burch, P., Burch, P., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavazo, D., Chen, G., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, N.J., Earnhart, C., Edgar, D., Edwards, C., Davy-Carroll, K.J., Earnhart, C., Edgar, D., Edwards, C., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, E., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., J., Li, J.
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Rattus norvegicus
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HTG; HTGS_PHASE1.
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Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabba Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/protein_id="AAF01242.1"
/db_xref="G1:6010761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Pred. No.
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9.4;
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                                Mohabbat, K.,
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AUTHORS
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oguh, M. Okwoonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pikens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tansey, J., Taylor, C., Taylor, T., Willalon, D., Vinson, R., Walli, R., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Watlingson, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Warles, K., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-SEP-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA

    * arbitrary. Gaps between the contigs are represented as
    * runs of N, but the exact sizes of the gaps are unknown
    * This record will be updated with the finished sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 25575 bases at least Q40 Consensus quality: 29587 bases at least Q30 Consensus quality: 29587 bases at least Q20 Estimated insert size: 11642; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0x in Q20 bases; agarose-fp estimation
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
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of Medicine,
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16928 17028 19302

gap of contig

of 2274

bp in length

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* 20635 20734: gap of unknown length
* 21742 21841: contig of 1007 bp in length
* 21842 21841: contig of 1007 bp in length
* 21842 23151: contig of 1107 bp in length
* 23152 23251: gap of unknown length
* 24577 25830: contig of 1125 bp in length
* 24677 25830: contig of 1125 bp in length
* 25831 25930: gap of unknown length
* 25831 27157: contig of 127 bp in length
* 25831 27157: contig of 1091 bp in length
* 27158 238348: contig of 1091 bp in length
* 28449 29550: contig of 1091 bp in length
* 29550 29559: qap of unknown length
* 29560 39579: contig of 1118 bp in length
* 29560 39777: contig of 1118 bp in length
* 30778 30877: gap of unknown length
* 30878 30877: gap of unknown length
* 30878 30877: gap of unknown length
* 29560 39759: contig of 1118 bp in length
* 30878 30877: gap of unknown length
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Result
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Maximum DB seq length: 200000000
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Perfect score:
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WPI; Yang F, 2000-116320/10. Macina RA, Sun ۲,

A new method for diagnosing, monitoring and staging lung cancer

Example 1; Pages 33-34; 40pp; English.

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entry)

Nucleotide sequence of Ω human Lng103 polypeptide

Human; lung specific gene; LSG; Lng103; cancer;

Homo sapiens

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                                          Sequences AAZ87205-Z87210 represent cDNAs encoding six human concurrent concerns associated proteins (NTAPs, AAY77121-Y77126). The present sequence, clone 2799056, encodes a putative odorant-binding correction, and was produced by extension of cDNA fragments isolated from a comman nasal polyp tissue cDNA library. The NTAPs are used for treatment correvention of neurological diseases (e.g., Alzheimer's, Parkinson's correction of cDNA library. The NTAPs are used for treatment corrections and the sequences of the correction of the 
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AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY9946 transmembrane and receptor PRO proteins can be used for screening potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequencoding then have various industrial applications, including uses
                                                                                                                       New mammalian DNA sequences encoding transmembrane, secreted PRO polypeptides, useful for screening of psmall molecule inhibitors of the relevant receptor/
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2000US-194647P
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(GETH J GENENTECH INC.

KP, Smith Chen Jith V, 'n, Watanabe Desnoyers atanabe CK, Ŀ, Wood Goddard ood WI, A, Godowski Zhang Z; PJ, Gurney ΑL;

P-PSDB; 2001-602746/68. DB; AAU29163.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals to screen for modulators of the compounds and

Claim 2; Fig 279; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR CC primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by CC comparing the level of expression of a PRO polypeptide in a test sample CC of cells from the animal and a control sample of normal cells, whereby a CC higher level of expression in the test sample indicates the presence of a CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, CC used to stimulate tumour necrosis factor (TNF) alpha release from human CC blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility to tumour development, particularly adrenal, lung, colon, CC susceptibility and can be used to determine the presence of tumours and also consest, prostate, rectal, cervical, or liver tumours, in mammalian cCC can be used for genetic analysis of individuals with genetic disorders.

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22-MAY-2000;
05-JUN-2000;
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01-SEP-1999;
29-CCT-1999;
30-NOV-1999;
16-DEC-1999;
16-DEC-1999;
05-JAN-2000;
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The present sequence represents a human lung cancer specific gene (LSG), and encodes a polypeptide designated Lng103. LSGs are useful in the treatment and diagnosis of lung cancer. The treatment and diagnosis of lung cancer which down regulates the expression of an LSG. An immune response can be mounted against a target cell expressing an LSG. Identification of potential therapeutic agents for use in imaging and treating lung cancer which comprises screening molecules for an ability to bind to or decrease expression of an LSG relative to LSG in the absence of the agent where the ability of a molecule to bind to the LSG or decrease expression of the LSG is indicative of the molecule being useful in imaging and treating lung
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Sequence 2036 BP; 477 Α. 586 Ç 528 ç 444 Τ; Н other;

Query Match
Best Local Similarity
Matches 1627; Conser

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Score 1457; DI Pred. No. 0; 0; Mismatches

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                                     novel
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  medical imaging;
                                human diagnostic protein #8511.
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 gene mapping; gene therapy;
maging; diagnostic; genetic |
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disorder;
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC afficeation, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                              ftp.wipo.int/pub/published_pct_sequences
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of mutations
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Sequence 2121 BP; 515 A; 583 C; 561 G; 462 Τ; 0 other;

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0 DВ

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Length

2121;

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ABA01989

The present invention provides the protein and coding sequences pf n human G-protein coupled receptors, designated NOVI, NOVZ, NOVZ, NOV3, NOV5a, NOV5b, NOV6b, NOV6b, NOV77, NOV8b, NOV9 and NOV10. These be used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoietic, developmental, retinal, feeding, neurological and psychotic diseases and disorders in the foreigns.

present sequence

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coding

sequence,

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gene

NOV4, These car

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Claim

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Page

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194pp;

English.

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infections

New G protein-coupled receptor related | for diagnosis, prevention and treatment neurodegenerative, retinal, immune, hem

hematopoietic polypeptides a t of metabolic,

disorders, and

diabetes,

polynucleotides

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30 MAR-2000
05-APR-2000
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5'UTR
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Gusev VY;
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antiarthritic;

receptor;

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ID AAF1827
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DT 14-b
XX Lung
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Best Local Similarity
Matches 682; Conserv
  cardioactive; immunomodulatory; muscular active; vulnerary, gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; r
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                                                       associated polynucleotide sequence SEQ
                                     cancer associated protein;
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ar active; vulnerary
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associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and cimmunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and peptide AAB58549 are used in the course of the invention for the sequences.
                                                                                                                                                                                                                                                                                                                                                          Lung cancer associated gene sequences, antigens, useful for treatment, prevent
                                                                                                                                                                                                                                                                                                             Claim 1; Page 732; 1425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-)
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P-PSDB; AAB58378.
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Sequence 1177 BP; 290 A; 361 C; 287 G; 239 Ŧ, 0 other;

Length 1177;

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Pred. No. 3.2e-243;
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16-JUN-1998;
16-JUN-1998;
22-JUN-1998;
22-JUN-1998;
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Soppet DR,
Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sspsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
                                                                                   New isolated human genes and the secreted \mu useful for diagnosis and treatment of e.g. disorders, immune diseases, inflammation or
                                             Claim
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re PA, Komat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC genes. This sequence represents a fragment of one of the human secreted convergences. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are consistent or gene therapy. Also pathological conditions, convergences by protein or gene therapy. Also pathological conditions can be compared by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new genes. Specific cuses are described for each of the 94 genes, based on which tissues they care most highly expressed in, and include developing products for the conditions or treatment of cancer, tumours, developmental abnormalities can foetal deficiencies, blood disorders, developmental abnormalities can foetal deficiencies, blood disorders, alzheimer's and cognitive considered solves, atherosclerosis, diabetes, cardiovascular disorders, kidney constructed in the construction of the sequences, shown in AAY86334 to AAY86585 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 642; Conserv
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                                                            gcaggtgaagccctcggccaatgaccaggagctgctagtcaagatccccctggacatggt
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 522; DB 21;
Pred. No. 9.9e-243;
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useful for preventing, treating or ameliorating medical conditions, can be considered by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new genes. Specific cor by determining the presence of mutations in the new genes. Specific cor are most highly expressed in, and include developing products for the corresponding to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes AAY86215 to AAY86333 are the secreted proteins encoded by the 94 human genes. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SN
Soppet I
Lafleur
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16-JUN-1998;
16-JUN-1998;
16-JUN-1998;
22-JUN-1998;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; cancer; Lumour, Jurian disorder; inflammat; foetal deficiency; blood disorder; immune system disorder; inflammat; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arrthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; didestive disorder; endocrine disorder; infection; AIDS; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 374; 586pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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, Brewer
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98US-0089510.
98US-0090112.
98US-0090113.
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   358 C;
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Carter KC, Mucenski M,
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   238
   Τ;
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Komatsoulis G;
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other;
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e disorder;
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Query Matcl Best Local Matches

Similarity

26 99

.4.8;

Score 436; DE Pred. No. 4.8e 0; Mismatches

DB 21; .8e-201;

Length 1172; Indels

0;

Gaps

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Conservative

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Match 636;

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AAH30554
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COMMENT ACT
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28-SEP-1998;
29-SEP-1998;
08-OCT-1998;
27-OCT-1998;
    (CHIR )
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                                                                                                                                                                                                                                                                                                                                                     detection;
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98US-0102180.
98US-0102380.
98US-0103815.
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12-FEB-2002

(first entry)

immune disorder; haematopoietic disorder; developmental disease; cances retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protech coupled receptor; cytostatic; antidiabetic; virucide; neuroprotective; nootropic; analgesic; antidepressant; antimigraine; anticonvulsant; neuroleptic; antiasthmatic; antiallergic; antiinflammatory; anorectic; antiarthritic antipsoriatic; antiatherosclerotic; antibacterial; fungicide; osteopathic; protozoacide; antiulcer; hypertensive; hypotensive; antiinfertility; vulnerary; nephrotropic; antilpemic; salivary gland protein; chromosome 20; ss.

antiarthritic

NOV6a; metabolic disorder; neurodegenerative disorder; disorder; haematopoietic disorder; developmental disea

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Best Local
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                               ABA01986 standard;
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Crkvenjakov R,
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dazzo F, Kennedy GC,
venjakov R, Dickson P
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30-MAR-2000;
30-MAR-2000;
05-APR-2000;
06-APR-2000;
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Shimkets
                                                                                        neurodegenerative, retinal, immune, obesity and infections -
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10-APR-2000;
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                                                                           Claim
                                                                                                     New G protein-coupled receptor related polypeptides and polynucleotides for diagnosis, prevention and treatment of metabolic,
                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                      mat_peptide
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DB; AAM47214.
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2000US-193339P
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Spytek K
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ev VY;
                                                                                               diabetes,
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The present invention provides the protein and coding sequences pf nove, human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4, NOV5, NOV56, NOV66, NOV6b, NOV7, NOV8b, NOV9 and NOV10. These or be used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoietic, developmental, retinal, feeding, neurological and psychotic diseases and disorders and infections. The present sequence is the NOV6a coding sequence, the gene for which is found on chromosome 20. The NOV6a protein shares homology

novel can

Sequence

963

BP;

217

314

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195

Η, 0 other with salivary gland

proteins. A;

Дb	QΥ	Вb	Qу	DЬ	Qy	Дδ	Qγ	Db	VΩ	Db	Qy	Db	Qy		
														Match	Query Match Best Local
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	783	acctcctagtgccatccctgcccaatctagtgaaaaaccagctgtgtcccgtgatcqaqq 622	acctcctagtgccatccctgcccaatctagtgaaaaaccagctgtgtcccgtgatcgagg 738	gcatccaactgctgcataagctctccttcctggtgaacgccttagctaagcaggtcatga 562	gcatccaactgctgcataagctctccttcctggtgaacgccttagctaagcaggtcatga 678	gtgcaagtggccccacccgcctggtcctcagtgactgtgccaccagccatgggagcctgc 502	gtgcaagtggccccacccgcctggtcctcagtgactgtgccaccagccatgggagcctgc 618	agaccatcgtggagttccacatgacgactgaggcccaagccaccatccgcatggacacca 442	agaccatcgtggagttccacatgacgactgaggcccaagccatccgcatggacacca 558	aggagotgotagtcaagatccocctggacatggtggotggattcaacacgcccctggtca 382	aggagctgctagtcaagatccccctggacatggtggctggattcaacacgcccctggtca 498	ggctgaaggtcatcacagctaacatcctccagctgcaggtgaagccctcggccaatgacc 322	ggctgaaggtcatcacagctaacatcctccagctgcaggtgaagccctcggcccaatgacc 438	vat	Query Match 24.1%; Score 405; DB 22; Length 963; Best Local Similarity 100.0%; Pred No. 5 1e-186.

Search completed: September 16, 2002, 06:31:11 Job time: $7619 \ \text{sec}$

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Result
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Maximum DB
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Perfect score:
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       Pred. No. score great and is der
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length: 2000000000
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US-08-715-568A-2
US-08-715-568A-2
US-08-712-702A-6
US-08-466-589-1
US-08-466-589-1
US-08-467-574-1
US-08-467-574-1
US-08-453-695A-111
US-08-453-702A-111
US-08-93-325-3
US-09-93-639-111
US-08-93-325-3
US-08-93-656-2
US-08-93-656-2
US-08-93-656-2
US-08-93-656-3
US-08-93-656-4
US-08-93-112
US-08-93-111
US-08-93-11
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US-08-715-568A-2
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Best Local S
Matches 21
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CITY: West
STATE: NJ
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Sequence 4, Appli					Sequence 27, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 4, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 14, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli

ALIGNMENTS

; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 7301 ; TYPE: DNA ; ORGANISM: Human US-09-816-088-3 Sequence 3, Application US/09816088
Patent No. 6326180
GENERAL INFORMATION:
APPLICANT: WEI, MING'Hui et al
TITLE OF INVENTION: ISOLATED HUMAN ENZYME, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING HUMAN ENZYME, AND USES THEREOF
FILE REFERENCE: CLORIBAL
CURRENT APPLICATION NUMBER: US/09/816,088
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4 Sequence 2, Application US/08715568A Patent No. 5856463 GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and
TITLE OF INVENTION: Treatment
NUMBER OF SEQUENCES: 14 COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC-DOS/M CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David,
STREET: 600 South Avenue |
CITY: Westfield 3365 gcccatttccctcagcattga 3385 785 gcccatttccctcagcattga 805 Similarity Conservative PC-DOS/MS-DOS 1.2%; Score 21; 100.0%; Pred. No. West 0; Littenberg, Krumholz Mismatches DB 4; 0.9; Uses ín Length 7301; & Mentlik Disease Indels 0; Gaps

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US-08-182-060A-6
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                            REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)992-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                       CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 92/06057
APPLICATION NUMBER: US 92/06057
FILING DATE: 24 JULY 1992
FILING DATE: 07/735,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                  APPLICATION NUMBER: 07/73
FILING DATE: 24 JULY 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn p.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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STREET: 1007 Market Street
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Local Similarity 100.0%; F
hes 19; Conservative 0;
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TYPE: nucleic acid
STRANDEDNESS: double
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Pred. No.
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INFORMATION FOR SEQ ID NO:
                                                                                                  APPLICATION NUMBER: 08/182,060
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 92/06057
FILING DATE: 24 JULY 1992
APPLICATION NUMBER: 07/735,066
FILING DATE: 24 JULY 1991
ATTORNEY/AGRET LINOFNAMION:
NAME: LINDA AXAMETHY FLOYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Patent No.
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Best Local
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                                               REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1032-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1394 catcatcactgagatcat 1411
                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
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LIBRARY: cDNA to mRNA
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OPERATING SYSTEM:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                  CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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STRAIN: Cultivar Wye
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(302)892-7949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard W. Pearlstein
                                                                                                                                                                                                                                                                                                           Macintosh
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                                                                                              AXAMETHY FLOYD
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Becker-Manley
                                                                                                                                                                                                                                                                                                                                                                                                                                     du Pont de Nemours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide Sequences
of Galactinol Synthase from Zucchini and Soybean
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Pred. No.
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26;
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Patent No.

TELEFAX:

Matches

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Best Local
                                                                                                                                                                                                           CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/ACENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
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APPLICANT: Elliot
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ORGANISM: Glycine max STRAIN: Cultivar Wye
                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUITITLE OF INVENTION: REV
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pair
                                                                                                                                                                       REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
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PUBLICATION INFORMATION: Unpublished
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LENGTH: 1406 base pairs
TYPE: nucleic acid
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                               FEATURE:
                                        MOLECULE TYPE:
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                                                     TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UFILING DATE: June 5,
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ZIP: 92101-2926
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              NAME/KEY:
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5837489
                                                                                               2068 base pairs
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Ellis, Steven B.
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CDS
166..1752
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100.0%; Pred. No.
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Best Local Similarity 100
Matches 18; Conservative
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                                                              Matches
                                                                          Query Match
Best Local S
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
APPLICATION NUMBER: US 08/
TAND DATE: 08-MAR-1993
                                                                                                                                                                                                                                                                                     TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1100 TCATCACTGAGATCATCC 1117
                1396 tcatcactgagatcatcc 1413
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 16-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Bru
STREET: 444 South Flower Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ellis, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                       LENGTH:
                                                              18;
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                                                            Similarity 100
18; Conservative
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                                                                                                                                                                                                                                                                       2068 base pairs
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166..1752
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100.0%; Pr
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26;
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RESULT 7 US-08-467-574-1

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US-09-217-345-1
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                                                                                                                                                                 GENERAL INFORMATION:
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                                                                APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: HARPOLD, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               1100 TCATCACTGAGATCATCC 1117
                                                                                                                                                                                                                                                                                                 1396 tcatcactgagatcatcc 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ellis, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Hatpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2068 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 638
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OPERATING SYSTEM:
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Similarity 100.0%;
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0; Mismatches
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; LOCATION:
US-09-217-345-1
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/466,589,

FILING DATE: 05-UN-95

PRIOR APPLICATION UNMBER: US 08/028,031

APPLICATION UNMBER: US 08/028,031

FILING DATE: 08-MAR-93

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REGISTRATION NUMBER: 24735-9949B
                                                                                                                                                                                                                                                                                                                                        Sequence 1, Applica Patent No. 5801232
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Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                APPLICANT: Ellist, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Halpold, Michael M.
TITLE OF INVENTION: HUMAN NEUBONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLO
                                                                                                                                                                                                                                                                                                                                                                                                                                        1100 TCATCACTGAGATCATCC 1117
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
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APPLICATION NUMBER: US,
FILING DATE: 21-DEC-98
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APPLICATION NUMBER:
FILING DATE: 05-JUN-
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                                                                                                                              STREET: 1660 Un:
CITY: San Diego
STATE: CA
                                                                                                          COUNTRY:
                                                                                                                                               ADDRESSEE: brown
                                                                                                ZIP:
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TOPOLOGY: bo
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                                                                                            RY: U.S.A.
92101-2926
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100.0%; Pred. No.
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     Version #1.25
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Gaps

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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

UMBER: US/08/496,855A 20-JUN-1995

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Best Local S
Matches 18
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GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALL...
STREET: 22.
CITY: Chicago
CTATE: Illinois
TTATE: IISA
                                                REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,695A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: No. 5708143and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
ADDRESSEE:
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les 18; Conserv
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                                                                                                                                                                                                                                                                                                                       60606
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100.0%; Pred. No.
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26;
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US-08-268-161A-111
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                                                       Query Match
Best Local S
Matches 18
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Best Local Similarity 100.0%; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 111, Application US/08268161A Patent No. 5798224
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                   1051 ttcctgagagtgcccatc 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1051 ttcctgagagtgcccatc 1068
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                                                                                                                                                                                      MOLECULE TYPE:
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562 TTCCTGAGAGTGCCCATC 579
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                                                       Local Similarity
les 18; Conserv
                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/
FILING DATE: June 27, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 233 Sc
CITY: Chicago
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LOCATION: 138..2528
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                                                                                                                                            NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                   TYPE:
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                                                     1.1%; Score 18;
100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
                                                       Mismatches
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26;
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26;
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RESULT 13
US-09-099-639-111
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                                                                                                                                                               Sequence 111, Application US/09099639 Patent No. 6262237
GENERAL INFORMATION:
APPLICANT: SUZUKI, Shintaro
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: Protocadherin Materials and Methods
NUMBER OF SEQUENCES: 115
                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                             1051 ttcctgagagtgcccatc 1068
                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                 APPLICANT: Suzuki, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HAM PC comparable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: NO. 5891706and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US
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TELEFAX: 25-3856
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                                                                              CITY:
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                                                 COUNTRY:
                                                                 STATE:
                                                                                          STREET:
                                                                                                      ADDRESSEE:
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LOCATION: 138
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                                                           Chicago
3: Illinois
                                     60606
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                                                                                 O'Toole, Gerstein, Murray, & cker, 6300 Sears Tower
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Pred. No
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOLAND, Greta E.
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             APPLICATION NUMBER: PCT/
FILING DATE: 23 DEC 1993
PRIOR APPLICATION DATA:
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suzuki, TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/263,161
FILLING DATE: 27 JUN 1994
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562 TTCCTGAGAGTGCCCATC 579
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LENGTH: 3033 base pairs
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                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          STREET: 6300 :
CITY: Chicago
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LOCATION:
                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Greta E. No. 6262237and REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1
CLASSIFICATION:
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6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki, Shintaro
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Pred. No.
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Query Match
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Watches 18; Conserve
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; LOCATION: 138..2528
PCT-US95-08071-111
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           CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/383,747
APPLICATION NUMBER: DE 40 31 758.7
FILLING DATE: 06-OCT-1990
PRIOR APPLICATION NUMBER: US 07/766990
PRIOR APPLICATION NUMBER: US 07/766990
APPLICATION NUMBER: US 07/766990
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235106
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KUIT G. BRISCOE
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 8297.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 111:
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LENGTH: 3033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Peter Schreier; Thomas Herget; and APPLICANT: Jeff Schell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 660 White
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
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OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
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(914) 332-1844
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100.0%; Pr
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; ORGANISM: Peanut (arachis hypogaea) US-08-903-325-3
Search completed: September 16, 2002, 06:24:15 Job time: 10628 sec
                                                                 В
                                                                                                                Query Match 1.1
Best Local Similarity 100.
Matches 18; Conservative
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                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         LENGTH: 3412 nucleott
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                    TOPOLOGY: Linear
                                                                                                                                                                                                                                                                          3412 nucleotides
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                                                                                                             1.1%; 5cc
100.0%; Pr
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length: 2000000000
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BI823956
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BI821769
BG529820
BE061388
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          BG530024
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BI824243
BF154920
BF154912
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BI772722
BG482718
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 BF095122
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B1823956 603039139
B1818205 603032679
B1811790 603035865
          BE933204
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BF154920
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                                           BG482718
BG530024
BG548906
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BF088537 RC1-HT08
BI772722 60305323
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                         RC1-HT088
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602502690
602558870
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RC1-HT088
RC0-BT081
RC0-BT081
PM3-UT005
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235	246	257	264	273	277	282	290	296	303	305	312	318	320	320	322	323	331	336	342	345	348	348	348	370	371	374	377
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287	318	428	397	836	743	. 353	343	482	429	379	363	630	912	556	365	390	370	438	525	433	785	642	640	957	469	463	1026
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BF804024	AW996310	BE932793	BE693858	BI820886	BG548174	BF089104	BE073529	BE926857	AW449208	BF088529	AW167610	BG482764	BG484717	BE933205	AW381927	BE829540	BE926678	AW167650	AL602621	BF826403	BG530180	BF672220	BG482968	BI822130	AI924632	BF743981	BI821994
	043-	BE932793 CM2-HT087		BI820886 603033924	BG548174 602575330	BF089104 CM0-HT091		BE926857 QV1-BT067	AW449208 UI-H-BI3-		AW167610 xn49e05.x	BG482764 602502549	BG484717 602505896	вЕ933205 RC1-HT088	AW381927 QV1-HT031	BE829540 RC0-ET007	BE926678 QV2-BT063	AW167650 xn47all.x	AL602621 DKFZp686K	BF826403 CM4-HN002	BG530180 602558678	BF672220 602150403	BG482968 602502981	BI822130 603039831	٤	\vdash	BI821994 603040023

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ALIGNMENTS

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REFERENCE AUTHORS TITLE JOURNAL ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT BI770190 COMMENT FEATURES DEFINITION Locus source BI770190 BI770190.1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 783)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc. BI770190 603053221F1 NIH_MGC_122 High quality sequence stop: Location/Qualifiers found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11508 row: i column: 06 Homo sapiens mRNA sequence. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5202893"
/clone_lib="NIH_MGC_122" /lab_host="DH10B" GI:15761768 Homo 783 bp mRNA linear EST 25-SEP-2001 sapiens cDNA clone IMAGE:5202893 5', Euteleostomi; be

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Query Match
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            ar EST 04-OCT-2001
IMAGE:5180336 5',
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BI823956.1 GI
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1449 row: m column: 09
High quality sequence stop: 793.
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Contact: Robert Strausberg,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 852)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
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Plate: LLAM11432 row: n column: 19
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/note="Organ: pooled brain, lung, testis; Vector: pcMV-SpORT6; Site_1: NotI; Site_2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5173842"
/clone_lib="NIH_MGC_115"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGATTCAACACGCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCC
                                                                                                                                 mRNA sequence.
BI821790
BI821790.1 GI:
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 784)
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603035865F1 NIH_MGC_115
                                                                                          Homo sapiens
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99.9%;
  Strausberg, Ph.D
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3.4e-295;
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tytyccaccagccatygyaycctycycatccaactyctycataagctctccttcctyyty
                                                        CAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTGAC
                                                                              caagccaccatccgcatggacaccagtgcaagtggccccacccgcctggtcctcagtgac
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Tissue Procurement: Life Technologies, Inc.
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Location/Qualifiers
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pcMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_115"
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/db_xref="taxon:9606"
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Pred. No. 3.5e-289;
0; Mismatches 1;
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                  122 agatggccggccgtggaccttcacccttctctgtggtttgctggcagccaccttgatcc 181
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1 (bases 1 to 955)

8 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAMI1440 row: 1 column: 09

High guality sequence from 764
AGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCC
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603035838F1 NIH_MGC_115 Homo
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Location/Qualifiers
                                                                                Conservative
                                                                                                                                                                                   /note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORTS; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                     /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176856"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                                                                              32.8%;
                                                                          Score 551; DB 10
Pred. No. 3e-270;
0; Mismatches
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                                                                                                                                                                                                                                                    mRNA sequence.
BG529820
BG529820.1 GI:
EST.
human.
                  cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1524 row: h column: 01
High quality sequence stop: 820.
Location/Qualifiers
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 826)
NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collect Unpublished (1999)
                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
 623
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                                                                                                                                               TGGATTCAACACGCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCA
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                                                                                                                                                                                                                                                                                                                                                                                  585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=qV0-BT0229-251
099-038-c01&t13-1999-10-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 620.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,m.K., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
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+55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: breast; Vector: pUC18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue stringency conditions."

a 161 c 214 g 144 t 1 others
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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99.7%;
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                                                                                                                                                                                                                                                                                                                   (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-HT0881-110900-024-d01&t3=2000-09-11&t4=1)
                                                                                                                                                                                                                                                                                                                                                         This sequence was derived from the FAPESP/LICR Human Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G., H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
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                               /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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/db_xref="taxon:9606"
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        Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11508 row: e column: 10
High quality sequence stop: 856.
Location/Qualifiers
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 945)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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603053235F1 NIH_MGC_122 Homo
                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:5202801"
/clone_lib="NIH_MGC_122"
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                                                                                                                                                                                                                                                                                                           CCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGAAAAGCTGACACAGGAGCTG
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Email: Capabs:reficiency, Fil. ..

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can l

found through the I.M.A.G.E. Consortium/LLNL at:

http://lmage.llnl.gov

Plate: LLCM1370 row: d column: 24

High quality sequence stop: 549.

Location/Qualifiers
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National Institutes of Health, M
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Eukaryota; M
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BG482718
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/Clone_lib="NIH_MGC_77"
/Clone_lib="NIH_MGC_77"
/Abb_host="DH10B (Tl phage-resistant)"
/Abb_host="DH10B (Clontage); Site_1: Sfil (ggccattatggcc); 5' and
/A daptor sequence: 5' -CACGGCCATTATGGCC_3' and 3' adaptor sequence:
/ATTCTAGAGGCCGACATGGGC_3' and 3' adaptor sequence:
/ATTCTAGAGGCCGACATGGGCG_3' and 3' adaptor sequence:
/ATTCTAGAGGCCGACATGGGC_3' and 3' adaptor sequence:
/ATTCTAGAGGCCGACATGGGCGGCGACATGGGC_3' and 3' adaptor sequence:
/ATTCTAGAGGCCGACATGGGC_3' and 3' adaptor sequence:
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/ATTCTAGGCC_3'                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
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/db_xref="taxon:9606"
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Pred. No. 2.1e-207;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG530024 602 bp mkna timedi 502558870F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4696865
                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: ATCC
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                  134
                                     /tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ACTGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library "
              Library.
a 202
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4696865"
/clone_lib="NHH_MGC_61"
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2:4696865 5',
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Query Match
Best Local Similarity
Matches 588; Conserv

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24.98;

Score 418; DB 10; Pred. No. 2.8e-202; 0; Mismatches 1;

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BG548906.1
                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cyapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                   BG548906 660 bp n 602575739F1 NIH_MGC_77 Homo sapiens mRNA sequence.
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 660)
                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                               Homo sapiens
                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCM1542 row: n column: 09
                                            quality sequence stop:
/organism="Homo sapiens"
/db_xref="taxon:9606"
                               Location/Qualifiers
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RC1-HT0881-290800-022-e03
BE933204
BE933204.1 GI:10459280
Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                               human.
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Query Match
Best Local Similarity
Matches 570; Conserv
actgtgccaccagccatgggagcctgcgcatc 623
                                                                                                                      cccaagccaccatccgcatggacaccagtgcaagtggccccacccgcctggtcctcagtg
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                                                                                               CCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCCTCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4703816"
/clone_lib="NIH_MGC_77"
/lab_bhost="DH10B (T1 phage-resistant)"
/lab_bhost="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCAATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACACGCGGCGCAATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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Pred. No. 4.5e-193;
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Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

524 bp 3 HT0881

Homo sapiens mRNA

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ctcggaagctcagttttacaccaaaggtgaccaacttatactcaacttgaataacatcag
                                                                                                                                                                                                GGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCT 257
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446; Conserv
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-RC1-HT0881-290 800-022-e03&t3=2000-08-29&t4=1) Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed low stringency conditions."
145 c 130 g 122 t
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/db_xref="taxon:9606"
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Pred. No. 4.8e-191;
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512; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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High quality sequence stop: 535.
Location/Qualifiers
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5181222"
/clone_lib="NIH_MGC_115"
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                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCO-BT0812-250
900-032-ell&t3=2000-09-25&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
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'note""Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196: 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                          /dev_stage="Adult"
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Search completed: September Job time: 8385 sec 16, 2002, 05:18:12

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Result
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Maximum Match 100%
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AT TOMBURDO	AAS72706	5330	AAI25947	AAK47474	AAK21316	ABA38468	ABA72883	AAI40226	AAI16752	AAK34508	AAK08624	ABA28591	ABA60344	AAC74887	AAI54231	AAI26228	AAK48404	AAK22236	ABA38963	ABA73788	AAI41191	AAI17050	AAK35477	AAK09583	ABA29112	ABA61288	AAT21378	AAL09812	848	AAC74959	(.)	AAZ97023	AAF18254	AAZ97114	198	ABA01989
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ALIGNMENTS

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A new method for diagnosing, monitoring and staging lung cancer
                               WPI; 2000-116320/10
                                                                                                                                                      prognosticate;
                                                                                                                                                                            Human lung specific gene-1
                                                                                                                                                                                                           AAZ29724;
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                                             Yang F,
                                                            (DIAD-) DIADEXUS LLC
                                                                            21-MAY-1998;
                                                                                          12-MAY-1999;
                                                                                                          25-NOV-1999.
                                                                                                                        WO9960160-A1
                                                                                                                                       Homo sapiens
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                                                                                                                                                                                           27-MAR-2000 (first entry)
                                            Macina RA,
                                                                            98US-0086212
                                                                                                                                                     lung cancer; diagnosis; ds.
                                                                                           99WO-US10344
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Example 1; Pages 33-34; 40pp; English.

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Sequences AAZ87205-Z87210 represent cDNAs encoding six human concurred to the construction of neurotransmission-associated proteins (NTAPs, AAY77121-Y77126). The present sequence, clone 2799056, encodes a putative odorant-binding component sequence, clone 2799056, encodes a putative odorant-binding component sequence, clone 2799056, encodes a putative odorant-binding component sequence of the construction of neurological diseases (e.g., Alabeimer's, Parkinson's component sequence, Alabeimer's, Parkinson's component sequence, Alabeimer's, Parkinson's component sequence of the construction of constr
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                                          lung
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Location/Qualifiers
163..1617
/*tag= a
/product= "Ing103"
                                          specific
                                                    of a human
                                                                 entry)
                                          gene;
                                                     Lng103
                                          LSG;
                                                     polypeptide
                                          Lng103; lung
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Best Local Similarity 99.7
Matches 1678; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New lung cancer -
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standard; cDNA; 1636

Дb

Oy Oy Oy

dd VQ

ρ γ

В 8

(UNQ706) cDNA sequence entry) SEQ IJ

PRO polypeptide; membrane bound protein; receptor; ambrane; secretion; immunoadhesion; pharmaceutical; diagnosis; screening;

NO:127.

99WO-US20111

98US-0098716,
98US-0098749,
98US-0098803
98US-0098803
98US-00998813
98US-0099556
98US-0099556
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22-FAR-2000
25-JAR-2000
05-JUN-2000
                                                                                                                                                                                                                                                The present sequence is the coding sequence for a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and meaning the protein and the protein sequence has applications.
                                                                                                                                                                                                                                  biology, incl
gene mapping.
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                                                                                                                                                                                                                                                                 Query Match 91.2%;
Best Local Similarity 99.2%;
Matches 1572; Conservative
                                                                                                                                                                                                                                                                                                                                                         Sequence 2121
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gagctgaaggaccacaacgccaccagcatcctgcagcagctgccgctgctccagtgccatg
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                                                                                                                                  ctgatcaatgaaaaggctgcagataagctgggatctacccagatcgtgaagatcctaact
                                                                                                                                                                                              atcgtgagtcaggacgtggtgaaagctgcagtggctgctgttgctctctccagaagaattc
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Homo sapiens.

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30-MAR-2000;
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06-APR-2000;
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11-APR-2000;
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14-APR-2000;
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 2000US-193305P.
2000US-193339P.
2000US-195343P.
2000US-195005P.
2000US-19508P.
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2000US-197081P.
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2000US-197087P.
2000US-197525P.
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79..150
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The present invention provides the protein and coding sequences pf. novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4, NOV5a, NOV5b, NOV6b, NOV7, NOV8a, NOV8b, NOV9 and NOV10. These can be used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoletic, developmental, retinal, feeding, neurological and psychotic diseases and disorders and infections. The present sequence is the NOV6b coding sequence, the gene for which is found on chromosome 20. The NOV6b protein shares homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Majumder
Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New G protein-coupled receptor related polypeptide
for diagnosis, prevention and treatment of metabol
neurodegenerative, retinal, immune, hematopoietic
obesity and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1035
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      catccgcatggacaccagtgcaagtggccccacccgcctggtcctcagtgactgtgccac
                                                                                                         catcogcatggacaccagtgcaagtggccccacccgcctggtcctcagtgactgtgccac
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                                                                                                                                                                                                                                                                                    9CCCtC99CCaatgacCaggagCtgCtagtcaagatCCCCCtggaCatggtcggctggatt
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DB; AAM47220.
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06; Conservative
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Spytek K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 A;
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Liu X, P
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Pred. No. 1.5e-199;
0; Mismatches 35;
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ırajan M,
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30-MAR-2000;
05-APR-2000;
06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NOV6a; metabolic disorder; neurodegenerative disorder; immune disorder; haematopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; syschotic disorder; G-protein coupled receptor; cytostatic; antidabetic; virucide; neuroprotective; nootropic; analgesic; antidepressant; antimigraine; anticonvulsant; neuroleptic; antiasthmatic; antiallergic; antiinflammatory; anorectic; antiarthritic; antiasthmatic; antiatherosclerotic; antibacterial; fungicide; osteopathic; protozoacide; antiuleer; hypertensive; hypotensive; antiinfertility; vulnerary; nephrotropic; antilipemic;
                                                                                                         30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4, NOV56, NOV66, NOV66, NOV60, NOV76, NOV86, NOV80 and NOV10. These cabe used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoietic, developmental, retinal, feeding, neurological and psychotic diseases and disorders and infections. The present sequence is the NOV6a coding sequence, the gene for which is found on chromosome 20. The NOV6a protein shares homology
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Lafleur
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CC The sequences shown in AAY86334 to AAY86585 represent fragments of the
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Local Similarity
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                                                                                  agccaccatccgcatggacaccagtgcaagtggccccacccgcctggtcctcagtgactg
                                                                                                                                                     tggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgagggcca
                                                                                                                                                                                                  ggtgaagccctcggccaatgamcaggagctgctagtcaagatccccctggacatggtggc
                                                                                                                                                                                                                    ggtgaagccctcggccaatgaccaggagctgctagtcaagatccccctggacatggtggc
                                                                                                                                                                                                                                                                                   caccgtcctgaagcacatcatctggctgaaggtcatcaccagctaacatcctccagctgca
                                                                                                                                 tggattcaacacgccctggtcaagaccatcgtggagttccacatgacgactgaggccca
                                                                                                                                                                                                                                                                                                                                    tgctcagtgccatgcgggaaaagccagccggagcatccctgtgctgggcagcctggtgaa
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                                                                                                                                                                                                                                                                                                                                                                                                                      aaaagctgacacaggagctgaaggaccacaacgccaccagcatcctgcagcagctgccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgatccaagccaccctcagtcccactgcagttctcatcctcggcccaaaagtcatcaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plated human genes and the secreted polypeptides they encode, for diagnosis and treatment of e.g. cancers, neurological ers, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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99.1%;
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Pred. No. 1.3e-156;
3; Mismatches 3;
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γΩ

53

ggagcgggccgaggactccagcgtgcccaggtctggcatcctgcacttgctgccctctga 112

Matches 648;

Conservative

0;

Score 635.8; Pred. No. 2.9e 0; Mismatches

..9e-J DB

Indels

1;

Gaps

1;

Query Match Best Local Similarity

37.8%; 99.5%;

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RESULT
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                                         associated proteins represented in AAB58106 - AAB5848. Lung cancer associated proteins and polynucleotide sequences, their agonists, and ansociated proteins and polynucleotide sequences, their agonists, and ansociated proteins and polynucleotive; cytostatic; cardioactive; and immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
   Sequence 1177
                                                                                                                                                                                                                                                                                              Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-587514/55
P-PSDB; AAB58378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antlinfective; gynecological; antlbacterial; diagnosis; neural disorder; immune disorder; proliferative disorder; wound healing; infectious disease; ds
                                                                                                                                                                                                                                                                                                                                                                     Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2000;
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ROSEN C A.
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  16-JUN-1998;
16-JUN-1998;
16-JUN-1998;
                                                                                                                                                                                                                                                                                       autoimmune disease; allergy; Alzheimer's disease; cognitive disorder schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
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98US-0089508.
98US-0089509.
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Sequence

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genes. This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides are cuseful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific cuses are described for each of the 94 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney clasorders, atherosclerosis, diabetes, cardiovascular disorders, kidney clasorders, digestive/endocrine disorders, infections and AIDS. The sequences shown in AAY86334 to AAY86585 represent fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998;
22-JUN-1998;
22-JUN-1998;
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DB; AAY86219.
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5.2e-155;
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The present invention describes a library of polynucleotides comprising 1079 nucleotide sequences (given in AAH30067 to AAH31145). Also described are: (1) an isolated polynucleotide (I) having at least 90% identity to one of the 1079 sequences; (2) a recombinant host cell containing (I); (3) an isolated polypeptide (II) encoded by (I); (4) an antibody that specifically binds to (II); (5) a vector comprising (I); and (6) a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell comprising detecting a gene product encoded by 50 the 1079 sequences given in the specification. The polynucleotides are used to monitor patients having (or susceptible) to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. The polynucleotides are also useful for monitoring the efficacy of various therapies and preventive
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29-SEP-1998;
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27-OCT-1998;
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Randazzo F, Kennedy GC, Pot D, Kassam
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
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Perfect score:
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      20054432
20054432
2005432
200543
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    Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-804-198-1
US-09-276-531-16
4 US-09-103-844A-2
US-09-130-114-2
US-08-910-991-7
US-08-910-991-7
US-08-471-033-39
US-08-471-044-39
US-08-471-044-39
US-08-471-046A-39
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7, Appli
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11, Appl
12, Appl
42, Appl
45, Appl
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1, Appli
16, Appl
12, Appli
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                       FEATURE:
NAME/KEY:
                                                          FEATURE:
NAME/KEY:
                                                LOCATION:
             LOCATION:
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28 37.2 2.2 1358 2 US-08-469-334-45 Sequence 45, Appl 37.2 2.2 1389 1 US-08-471-033-27 Sequence 27, Appl 37.2 2.2 1389 2 US-08-471-044-27 Sequence 27, Appl 37.2 2.2 1389 2 US-08-471-044-27 Sequence 27, Appl 37.2 2.2 1389 2 US-08-471-046A-27 Sequence 27, Appl 37.2 2.2 1389 2 US-08-470-566B-27 Sequence 27, Appl 37.2 2.2 1389 2 US-08-469-334-27 Sequence 27, Appl 37.2 2.2 1389 3 US-09-300-529-27 Sequence 27, Appl 37.2 2.2 1395 3 US-08-435-069-3 Sequence 3, Appl 37.2 2.2 1995 1 US-08-417-0444B-3 Sequence 3, Appl 37.2 2.2 4031 2 US-08-471-044-49 Sequence 49, Appl 41 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 42 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 43 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 43 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 44 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 44 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 44 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 44 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 44 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl 45 37.2 2.2 4031 3 US-09-300-529-49 Sequence 49, Appl 45 37.2 2.2 4031 3 US-09-300-529-49 Sequence 49, Appl 45 37.2 2.2 4031 3 US-09-300-529-49
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ALIGNMENTS

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COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804, 22
FILING DATE: FEBRUARY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ. ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08804227C Patent No. 5876991 GENERAL INFORMATION:
                                                                                                                           MOLECULE TYPE:
FEATURE:
NAME/KEY: CD:
LOCATION: 35
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: LILLY CORPOI
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                             CDS
14046..20036
                                                                                                                             CDS
350..14002
                                                                                                                                                                                                              linear
20110..31284
                                                                                                                                                                                        DNA (genomic)
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US-08-804-227C-7
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Best Local Similarity
Matches 107; Conserv
                                                                                                                 REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43721 CGGACGGGAGATCCCCGGGGCCGGAGCGGTCGGGGGGCGCGACGGACCGCACCTGGCGCT 43780
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                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROSTECK, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
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                                                                     STRANDEDNESS:
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   NAME/KEY:
LOCATION:
                                                            TOPOLOGY:
                                                                                    LENGTH: 44377 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                     COMPUTER: Macinto OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PAUL R. CANTRELL 1: STREET: LILLY CORPORATE CENTER
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LOCATION:
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                                                                                                                                                                                 CANTRELL, PAUL R.
                                                                                                                                                                                                                                                                                                                                                                                                         INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                   46285
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CDS
350..14002
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Richardson, Mark
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31329..36071
                                        DNA (genomic)
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Pred. No. 0.5;
0; Mismatches 109;
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RESULT 3
US-09-276-531-16
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US-08-804-198-1
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Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43721 CGGACGGGAGATCCCCGGGGCCGGAGCCGCTCGGGGGCGCCGACGGACCGCACCTGGCGCT 43780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOUTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES.

TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH OUMBER OF SEQUENCES: 134

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43661 CCTCGAACTCGGCGGCCGGCTGGATCACCGCCGACGACGACGTCGTGGTGCTGGCCGCCGC 43720
 ATTORNEY/AGENT II
NAME: Lynn E.
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
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                                 CLASSIFICATION:
                                                   FILING DATE:
                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                        STREET: 3174 PORTER DRIVE CITY: PALO ALTO
                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                           CALIFORNIA
                                                                                                                                                                                                                                                            USA
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Hillman, Jennifer
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31329..36071
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INFORMATION:
                                                March 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5%;
                                                               60/079,677
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Pred. No. 0.5;
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                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                         APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4245 base pairs
TYPE: nucleic acid
                                TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY: BRAITUT21
CLONE: 2526432
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REFERENCE/DOCKET NUMBER: PA-0008 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          490 GACAAGTTCCCCGAGGGGGACGTCTGCATC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 gtgaagccctcggccaatgaccaggagctgctagtcaagatccccctggacatggtggct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccaccatccgcatggacaccagtgcaagtggcccacccgcctggtcctcagtgactgt
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at various positions throughout the sequence
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Pred. No. 0.55;
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US-09-130-114-2
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LENGTH: 1931
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APPLICANT: Horlick, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3%;
Best Local Similarity 43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09130114 Patent No. 5976807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291328 GACGATGCCGTCGACAAGATCAGCGAGCACCTGCGCGACCACCGCTGGCAAGGCCGAC
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291268 ATCCTGGTCAAC 291257
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631 tgcataagctctccttccttggtgaacgccttagctaagcaggtcatgaacctcctagtgc
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                                                                     ccacccgcctggtcctcagtgactgtgccaccagccatgggagcctgcgcatccaactgc
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                                                  tegtecteccegtecteccegtecteccegtecteccegtectectegtectecceg
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US-08-804-166-7
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                                                                                                                                                                                                                        Query Match
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ATTORNEY/AGENT INFORMATIONNEY/AGENT INFORMATION: BLOWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPE
TELECOMMUNICATION INFORMATION:
"PELEPHONE: (202) 638-5197
"PELEPHONE: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08804166 Patent No. 6193972
GENERAL INFORMATION:
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                                      403
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
                                                                   916
                                                                                               343
                                                                                                                    856 CAGCTGGTGCTGGTCCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGG
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US
FILING DATE:
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APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1301 base par
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                        Local
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SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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CCCGCGTGCTGCAGGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTG 1019
                     tcctccagctgcaggtgaagccctcggccaatgaccaggagctg 446
                                                        GCTGCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCCACCATGA
                                                                               gcagcctggtgaacaccgtcctgaagcacatcatctggctgaaggtcatcacaggctaaca 402
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                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                         linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                   2.2%; 51.8%;
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                                                                                                                                                                                 Score 37.6; DI
Pred. No. 1.1;
0; Mismatches
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US-09-434-288-11; Sequence 11, A
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                             RESULT
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US-08-910-991-7
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/011

FILING DATE: 20 February

ATTORNEY/AGENT INFORMATION:

NAME: YUN, Allen C.

REGISTRATION NUMBER: 37,97
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 737-352
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CATELECOMMUNICATION INFORMATION:
                                                                     976
                                                                                                                                                      343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROT.
NUMBER OF SEQUENCES: 22
                                                                                 403 tcctccagctgcaggtgaagccctcggccaatgaccaggagctg 446
                                                                                                                            916
                                                                                                                                                                            856 CAGCTGGTGCTGCTCCACGGTGCCGCCCCATCAATGCCACCCTGGCTGTGGAGAAGGAGG 915
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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                                                                                                                      GCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGA 975
                                                                                                                                        gcagcctggtgaacaccgtcctgaagcacatcatctggctgaaggtcatcacaggctaaca 402
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419 Seventh Street N.W.,
                                                                                                                                                                                                                                       Conservative
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HYBRID PROTEINS
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                                                                                                                                                                                                                                    Score 37.6; DB 4; Length 1301; Pred. No. 1.1; 0; Mismatches 79; Indels 0
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Application US/09434288

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SEQ ID NO 11
LENGTH: 3241
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR APPLICATION NUMBER: 1098-11-05
PRIOR FILING DATE: 1998-11-05
NUMBER: 05 SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atent No. 5770696
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Betlach C., APPLICANT: McDaniel, F
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                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                            SOFTWARE: PatentIn Relacement APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                      APPLICANT: Estruch, Juan J
TITLE OF INVENTION: NO. 5770696el Pesticidal Proteins
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                 CITY: Hawthorne
                                                                                                                                                                COUNTRY: U
ZIP: 10532
                                                                                                                                                                                                                                    ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
CLASSIFICATION:
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Koziel, Michael G
Mullins, Martha A
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                                                                                                                                                                                                                                                                                                                                             Duck, Nicholas B
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                                US/08/471,033
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Pred. No. 1
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                                                                                                                                                                                                                                                                     RESULT 10
US-08-471-033-42
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                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Warren,
APPLICANT: Koziel,
APPLICANT: Mullins
                                                                                                                                                                                                                                      Sequence 42, Application US/08471033 Patent No. 5770696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                 APPLICANT:
                             APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins
NUMBER OF SEQUENCES: 50
                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
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APPLICATION NUMBER: US 08/314,594
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LOCATION: 9..1238
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         473
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                                                                                                                                                                                                                                                                                                                                                         533 ccaagccaccatccgcatggacaccagtgc
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REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SQLv3
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ggctggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcaggtgaagccctcggccaatgaccaggagctgctagtcaagatccccctggacatggt 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
                                                                               Carr, Brian
Desai, Nalini M
Kostichka, N. Kristy
Duck, Nicholas B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                    Mullins, Martha
                                                                                                                                                 Nye, Gordon J
                                                                                                                                                                                      Koziel, Michael
                                                                                                                                                                                                    Warren,
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CIBA-GEIGY Corporation
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                                                                                                                                                                   Gregory W
Michael G
, Martha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Maize optimized DNA sequence encoding VIP2A(a) with the removed as contained in pCIB5527"
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Pred No. 1
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                                                  Strains
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7 Skyline Drive

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RESULT 11
US-08-471-044-39
; Sequence 39, Application US/08471044
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.2%;
Best Local Similarity 48.6%;
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ZIP: 10532
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYPEM: PC-DOS/MS-DOS
THE ASSE #1.0,
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TELEPHONE: 919-541-8582
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 42:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1241 base pairs
TYPE: nucleic acid
                                                                                                                      533 ccaagccaccatccgcatggacaccagtgc
                                                                                                                                                                275 CATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCCTGACCGA 334
                                                                                                                                                                                                               473
                                                                                                                                                                                                                                         215 CGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAG 274
                                                                                                                                                                                                                                                                     413 gcaggtgaagccctcggccaatgaccaggagctgctagtcaagatccccctggacatggt 472
                                                                                                                                                                                                                                                                                                                    155 GAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCTTCGAGGA 214
                                                                                                                                                                                                                                                                                                                                          353 gaacaccgtcctgaagcacatcatctggctgaaggtcatcacagctaacatcctccagct 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 9.1238
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                            335 GGGCAACACCATCAACAGCGACGCCATGGC
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 23-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/314,594 FILING DATE: 09-SEP-1994
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                                                                                                                                                                                       99ctggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgaggc 532
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/desc = "Synthetic
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25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion signal removed and the eukaryotic secretion signal inserted as contained in pCIB5528"
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                                                                                                                                                                                                                                                                                                                                                                                               Score 37.2; DB 1; Length 1 Pred. No. 1.3; o; Mismatches 108; Indels
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                                                                                                                                  562
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1241;
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353 gaacaccgtcctgaagcacatcatctggctgaaggtcatcacagctaacatcctccagct 412

GAACGACATCAAGACCAACTACAAGGAGATCACCTTCAGCATAGCCGGCAGCTTCGAGGA 214

Matches 102; Query Match Best Local Similarity

Conservative

0;

Score 37.2; DB 2; Pred. No. 1.3; 0; Mismatches 108;

Length 1241; Indels

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Gaps

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OTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: ; OTHER INFORMATION: r US-08-471-044-39
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
                                                                                                                        HYPOTHET ICAL:
                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-SEP-
                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 06-JUN-19
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TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 25-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08 FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                  nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                         Pace,
                                                                                                                                                                                                                  1241 base pairs
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                                                                                         CDS
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Koziel, Michael
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                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                         Gary M.
                                                                                                                                                                                                                                                                                                                                                                       JMBER: US 08/037,057
25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nalini M
                         /note= "Maize optimized DNA sequence encoding VIP2A(a) with the Bacillus secretion sig removed as contained in pCIB5527"
                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/218,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/463,483
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                                                                                                                                                                                                                                                                                         40,403
SER: CGC 1695/CIP3/DIV6 -
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US-08-471-044-42
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                                                                                                      TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
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APPLICANT:
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PRIOR APPLICATION DATA:
US 08/463,483
                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-SEP-PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 23-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
                  TOPOLOGY: 1
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                              REGISTRATION NUMBER: 40,403 REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 25-MA
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   DESCRIPTION:
                                                   STRANDEDNESS:
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                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggctggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgaggc 532
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                                                 nucleic acid
DEDNESS: single
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Kostichka, N. Kristy
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Koziel, Michael G
Mullins, Martha A
                                                                                                                                         919-541-8689
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                                      linear
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                                                                                                                                                                                                                                 Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1995
                                                                                                                                                                                                                                                                    UMBER: US 08/037,057
25-MAR-1993
                                                                                                                                                                                                                                                                                                                       23-MAR-1994
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other nucleic acid
/desc = "Synthetic
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   DNA"
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                                                                                       APPLIANCE DATE:
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                 FILING DATE: 09-SEP-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/463,483A
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                               FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
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TITLE OF II
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                            CITY:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
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10532

23-MAR-1994

US 08/218,018

US 08/314,594

USA

Hawthorne NY

f: Estruch, Juan J
INVENTION: No. 5849870el Pesticidal Proteins

and

Strains

Duck, Nicholas B

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; NAME/KEY: CDS
; LOCATION: 9.1238
; OTHER INFORMATION:
                                                                                                                                                                            US-08-463-483A-39
                                                                                                                                                          Sequence 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                         GENERAL INFORMATION:
 APPLICANT:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                      ggctggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgaggc 532
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                                                                                                                                                                                                                                                                                                                     CATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCCTGACCGA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102;
                                                                                                                                                           Application US/08463483A
Carr, Brian
Desai, Nalini M
Kostichka, N. Kristy
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                                                                                      Warren, Gregory
Koziel, Michael
                                                      Nye, Gordon J
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                                                                      Martha
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                                                                      ⊅ G ₹
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Pred. No. 1
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US-08-463-483A-42
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                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42,
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Best Local :
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APPLICANT:
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INFORMATION FOR SEQ ID NO: 39:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                  APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                  APPLICANT:
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LOCATION: 9..1238
CTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LENGTH: 1241 base pair
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                                                                                                     CITY:
STATE:
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 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                              ADDRESSEE: CIBA-GEIGY CO
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                      ZIP:
                                                                                   COUNTRY:
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Local Similarity 48.6%;
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STRANDEDNESS: single
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REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGO
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Koziel, Michael (
Mullins, Martha /
Nye, Gordon J
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Desai, Nalini M
Kostichka, N. Kristy
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PC-DOS/MS-DOS
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Michael G
Martha A
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Pred. No. 1.
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APPLICANT: APPLICANT: APPLICANT: APPLICANT

Desai, Nalini M Kostichka, N. Kı Carr, Brian Nye, Gordon J Mullins, Martha

Kristy

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US-08-471-046A-39
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          Sequence 39, Application US/08471046A Patent No. 5866326
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION:
OTHER INFORMATION:
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TELEPHONE: 919-541-8615
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
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                                                                                                                                                                        335 GGGCAACACCATCAACAGCGACGCCATGGC
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                        CGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAG 274
                                                                                                                                                                                                                                                                                                                                gcaggtgaagccctcggccaatgacccaggagctgctagtcaagatccccctggacatggt 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%;
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Pred. No. 1.3;
0; Mismatches 108;
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FILING DATE: 23-MAR-1994

PRIOR APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: GCG1695/CIP3/DIV8 - SQLV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
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PRIOR APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-UW-1995
PRIOR APPLICATION NUMBER: US 08/314,594
EXITING DATE: US 08/314,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5866326artis Corporation
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                   473 ggctggattcaacacgcccctggtcaagaccatcgtggagttccacatgacgactgaggc 532
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275 CATCATCACCTACAAGAACGTGGAGCCCACCACCATCGGCTTCAACAAGAGCCTGACCGA 334
                                                                          215 CGAGATCAAGGACCTGAAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAG 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U. ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                             /note= "Maize optimized DNA
sequence encoding VIP2A(a) with the Bacillus secretion signa
removed as contained in pCIB5527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/471,046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39:
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                              Score 37.2; DB 2;
Pred. No. 1.3;
0; Mismatches 108;
                                                                                                                                                                                                                                                    DB 2; Length 1241;
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                  0;
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Search completed: September 16, 2002, 03:26:41 Job time: 9324 sec

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Database :
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                     O
                                                                                                 C
                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    Score
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length: 2000000000
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(SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:*

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315
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taaacactgactcagatttt.....tgtgtattatctacttatgc 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1986.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2011.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2011B.DAT:*
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                            AAZ 297 25
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ABA 19145
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                                                                                                                                                                                                                                                 Description
Human reproductive
Genomic sequence #
Human immune/haema
                                                                       Human nervous syst
Human musculoskele
Human musculoskele
                                                                                                                                                     Murine Ataxia-tela
                                                                                                                                                                       ACNPV genomic DNA
                                                                                                                                                                                                Human lung specifi
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ίς. `	ALIGNMENTS					
Human reproductive	AAL04555	22	21403	5.4	17	4 4
reproducti	AAL04554	322	19802	n (Ji	17	43
-	AAK90892	22	15866	5.4	17	42
0	AAZ36757	21	12151		17	41
	ABL07088	23	9931	5.4	17	40
	ABL20966	23	8031	5.4	17	39
Drosophila melanog	ABL23206	23	6236		17	ω (80 ·
CUNA sequence of P	AAF83913	21	5534	л U	17	35 37
Human PCTA-1 splic	AAA10226	21	5408		17	, W
Drosophila melanog	ABL18530	23	5407	5.4	17	34
CO.	AAF83912	22	5406	5.4	17	33
	AAS35981	22	4646	5.4	17	32
0	AAS35982	22	4645		17	31
to	AAT09026	17	4146		17	30
	ABL07106	23	4060	5.4	17	29
	ABL21898	23	3424		17	28
	ABL20736	23	3241		17	27
	ABL02390	23	3201	5.4	17	26
	ABL21896	23	3008		17	25
₃ .	ABL27076	23	2879	5.4	17	24
	AAC36512	21	2388	5.4	17	23
dopsis thali	AAC51459	21	2385		17	22
#3985 1284 HODE #421/ USEU C	APPEDIAA) L	1959	л с 2-4	17	210
#4079 for g	AAI14146	2 0	1959		17	19
bone m	AAK29571	22	1959	5.4	17	18
brain	AAK04090	22	1959	5.4	17	17
#4012 f	ABA25546	22	1959		17	16
foetal	ABA55872	22	1959		17	15
breast	ABA45382	22	1959		17	14
Human foetal cDNA,	AAH94373	22	1239		17	13
otide		21	842	51 (17	12
	242	3 :	726	л (-	17	1;
Human inflammatory	AAH92576	22	669	л.	17	10

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0 0 0 0 0 0 0

RESULT
AAZ29725
ID AAZ2 21-MAY-1998; WO9960160-A1 Homo sapiens Lung Specific Gene; LSG; human; diagnostic marker; prognosticate; lung cancer; diagnosis; ds. Human lung specific gene-2. 27-MAR-2000 AAZ29725; AAZ29725 standard; 12-MAY-1999; 25-NOV-1999 (DIAD-) DIADEXUS LLC. Ή, Macina RA, (first entry) 98US-0086212 99WO-US10344 DNA; Sun 315 ВP

A new method for diagnosing, monitoring and staging lung cancer 2000-116320/10.

Example 1; Page 35; 40pp; English.

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RESULT
AAT13635/
ID AAT1
XX AAT1
XX AAT1
XX AAT1
XX AUN
XX
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Best Local S
Matches 315
            sequence
                                                                                                                                                                                                                                                       04-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Autographa californica nuclear polyhedrosis virus clone disruption; non-essential gene; heterologous protein pro expression vector; baculovirus; ss.
                                     Autographa
                                                                                     GENBANK;
                                                                                                                                                                                                                                                                                                    30-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                    18-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autographa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1996
                                                                                                                                                                                                        (NATU-) NATURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT13635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 315 BP;
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315; Conserv
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                                                                                       L22858
                                                                                                                                                      Bishop D,
californica nuclear polyhedrosis virus complete genome useful in the prodn. of vectors for enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                 californica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                     94GB-0013420
                                                                                                                                                                                                                                                                                                    95WO-IB00578
                                                                                                                                                                                                     ENVIRONMENT RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 A; 58 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 133894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 315; DB 21;
Pred. No. 7.5e-151;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 G; 100 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315;
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Query Match
Best Local Similarity 100.
                                                                                                                                                      28-JUL-1995;
16-MAY-1995;
21-JUN-1995;
                    carriers
                                                               WPI; 1997-012074/01.
P-PSDB; AAW36178.
                                          New gene
                                                                                                 Collins
                                                                                                                      (UYRA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete nucleotide sequence of the genome of clone 6 of the baculovirus Autographa californica nuclear polyhedrosis virus (AcNPV) has been determined. The sequence is taken from the Genbank record L22858. The patent specification claims a polynucleotide selected from open reading frames (ORFS 13, 20, 22-26, 28-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-126, 129-130, 140-146, 148-150, 152 and 154 from a total of 154 ORFS identified by the patentees. See T13636-731. Expression vectors conty. the complete genomic sequence of AcNPV, with the exception that at least one nonessential ORF is disrupted or replaced are useful for the synthesis of patents.
                                                                                                                                                                                                   16-MAY-1996;
                                                                                                                                                                                                                                             WO9636695-A1
                                                                                                                                                                                                                                                                                                                                      mouse;
                                                                                                                                                                                                                                                                                                                                              phosphatidylinositol-3
                                                                                                                                                                                                                                                                                                                                                      Ataxia-telangiectasia; A-T; mutated; ATM; 11q22-23; signal transduction; DNA damage; cell cycle control; screening; gene therapy; catalytic;
                                                                                                                                                                                                                                                                                                                                                                                           Murine
                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT45424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT45424 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 133894 BP; 39195 A; 27151 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heterologous proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heterologous protein expression, interferon(s) and neurotoxin(s)
                               useful
                                                                                                                                                                                                                                                                                                                musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                 FS,
                                                                                                                                                                                                                                                                                                                                      SS
                                                                                                                                                                                                                                                                                                                                                                                         Ataxia-telangiectasia ATM gene.
                                                                                                                    UNIV RAMOT APPLIED RES
US DEPT HEALTH & HUMAN
                              in
                                         ATM implicated in
                             screening
                                                                                                Shiloh
                                                                                                                                                      95US-0508836.
95US-0441822.
95US-0493092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and neurotoxin(s)
                                                                                                                                                                                                   96WO-US07040
                                                                                                                                                                                                                                                                   Location/Qualifiers
42..9242
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90-186; 122pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                              methods,
                                                                                                                                                                                                                                                                                                                                              kinase; PI-3; cancer
                            ataxia-telangiectasia and related ods, partic. for identifying diseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 21;
Pred. No.
                                                                                                                      & IND DEV
SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27347 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interleukin(s),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                             predisposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 133894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                              carrier;
                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Example 4; Page

90-95;

127pp;

English

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CC This sequence represents the mouse ATM gene, mutations in which cause CC ataxia-telangiectasia (A-T), a progressive genetic disorder affecting CC the Central nervous and immune systems. In the human ATM gene, there is CC extensive alternate splicing at the 5' UTR of the ATM transcript giving CC first exon in the human sequence is designated lb. An alternative leader CC exon, la is given in AAT45421 and the 3' UTR is in AAT45421). The CC gene, located in humans at chromosome 11q22-23, is probably involved in a CC novel signal transduction system that links DNA damage surveillance to CC cell cycle control. This murrine sequence is located in chromosome 9, band CC cell cycle control. This murrine sequence for CC cell cycle control. This murrine sequence is located in chromosome 9, band CC terminal region showing high sequence homology to the catalytic domain CC of phosphatidyllnositol-3 kinases. A-T mutations affect a variety of tissues and lead to cancer predisposition. Identification of A-T CC carriers, by analysis at nucleic acid or protein levels, allows better csupervision and treatment of such subjects who are at increased risk of developing cancer and are particularly sensitive to raddation. The CC human disease. Also viral vectors expressing the ATM protein can be used cin cance theraps of A-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
04-FEB-2000
04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
17-MAR-2000
07-JUN-2000
28-JUN-2000
07-JUN-2000
07-JUL-2000
07-JUL-2000
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                                                                                                                                                                                                                          WO200159063-A2
                                                                                                                                                                                                                                                  Ното
                                                                                                                                                                                                                                                                                  antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidlabetic; antiulcer; anticonvulsant; antifungal;
antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                     Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
                                                                                                                                                                                                                                                                                                                                                                        Human nervous
                                                                                                                                                                                                                                                                                                                                                                                                                         ABA19145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA19145
                                                                                                                                                                                                                                                                         neurological disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9620 BP; 2898 A; 1931 C;
                                                                                                                                                                         17-JAN-2001;
                                                                                                                                                                                                 16-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tctcttagagatctacag 6088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy of A-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
2000US-0179065
2000US-0180628
2000US-0184664
2000US-0186350
2000US-019974
2000US-0199123
2000US-0198123
2000US-025515
2000US-025515
2000US-02515
2000US-0215135
2000US-0216486
2000US-0216647
2000US-0216880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                         2001WO-US01334
                                                                                                                                                                                                                                                                                                                                                                        system related
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        polynucleotide SEQ ID
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                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                       NO 11476.
                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                        ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
  14-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
21-CCT-2000
02-CCT-2000
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12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
2000US-0217487
2000US-0217487
2000US-0225963
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225266
2000US-0225277
2000US-022577
2000US-022577
2000US-0225776
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2000US-02257868
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2000US-0229987
2000US-0239984
2000US-0239987
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2000US-0239987
2000US-0239987
2000US-0239987
2000US-0239987
2000US-0239987
2000US-0239987
2000US-0239987
2000US-0239997
2000US-02399937
2000US-0241786
2000US-0241786
2000US-024181808
2000US-024181808
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Вb

Qy

0;

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune
                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000
01-NOV-2000
08-NOV-2000
01-NOV-2000
01-DEC-2000
                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                      useful
                                                                                                                                                                                                                                 Nucleic
                                                                                                                                                                                                                                                                                                                          ( HUMA - )
                                                                                                                                                                                                                      for
                                                                                                                                                                                                                 acids encoding for preventing,
                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                   SEQ
                                                                                                                                                                                                    metastases
                                                                                                                                                                                                                                                                                                                                                  2000US-024221.
2000US-0244617.
2000US-0246476.
2000US-0246478.
2000US-0246478.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246613.
2000US-0246611.
2000US-0249207.
2000US-0249207.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249211.
2000US-0249216.
2000US-0251166.
                                                                                                                                                                                                                                                                                                                          GENOME
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                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                       SCI INC
                                                                                                                                                                  11476;
                                                                                                                                                                                                             diagnosing
                                                                                                                                                                                                                                                                                           Ruben
                                                                                                                                                             1701pp + Sequence Listing;
                                                                                                                                                                                                                                                                                           SM;
                                                                                                                                                                                                            nervous system antigen polypeptides, and/or treating nervous system
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marrow, bre (b) immune haemolytic

disorders e.g. Addison's disease, anaemia, autoimmune thyroiditis,

diabetes

mellitus,

English

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RESULT
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Best Local
 18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-JUL-2000;
14-AUG-2000;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          antiallergic; hepatotropic; antidiabetic; vulnerary; anticonvulsant; antibacterial; cardiant; gene therapy; cancer; immune dis
                                                                                                                                                                                                                                                                                                                                                                                                                                cardiant; gene therapy; cancer; neurological disease; infection;
                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                         WO200155367-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      musculoskeletal system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human musculoskeletal system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL36171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAL36171 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23934 BP; 7785 A; 4761 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
2000US-0179065.
2000US-0180628.
2000US-01806360.
2000US-0189874.
2000US-0199123.
2000US-0199123.
2000US-0214866.
2000US-021486.
2000US-021486.
2000US-0216647.
2000US-021680.
2000US-021680.
2000US-021749.
2000US-021749.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-021890.
2000US-0225214.
2000US-022526.
2000US-025266.
2000US-022526.
2000US-022526.
2000US-022526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                             2001WO-US01338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                      ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G; 7023 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; antiulcer;
antifungal; antiparasitic;
sorder; cardiovascular disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 23934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (antjagonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC (c) gastrointestinal tract, liver, lung, or urogenital; (b) immune CC (ascrointestinal tract) in the diagnosis, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC (c) infectious diseases such as viral, bacterial, fungal and CC parasitic infectious diseases such as viral, bacterial, fungal and CC parasitic infections.

CC (c) from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
Sequence 23934 BP;
                                                                                                                                                                                                                                                                                                                                                       Example
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-451937/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                         SEQ
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2000US -0246611
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2000US -0246613
2000US -02496611
2000US -0249207
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2000US -0249211
2000US -0249214
2000US -0249215
2000US -0249216
2000US -025921
2000US -025922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENOME
                                                                                                                                                                                                                                                                                                                                                         ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC,
7023 A; 4365 C;
                                                                                                                                                                                                                                                                                                                                                      2536; 781pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS
4761 G;
7785 T; 0 other;
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14-AUG-2000
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18-AUG-2000
18-AUG-2000
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23-AUG-2000
23-AUG-2000
20-SEP-2000
01-SEP-2000
01-SEP

2000US-0225757
2000US-0225758
2000US-0225759
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2000US-02346524
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2000US-02346526
2000US-02346526
2000US-02346526
2000US-0236527

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E N	Guery Match Best Local Similarity 100.0%; Pred No. 22; Length 23934; Watches 18; Conservetive 0; Mismatches 0; Indels 0; Gaps 0; Val 72 ciacasattitigaaania 189 Db 1308 CTACAANTTTOMANIA 13041 EESULT 6 WALSELT9 WALSELTS WALSELTS WALSELTS
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	01-SEP-2000 05-SEP-2000 06-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 08-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 21-SEP-2000 22-SEP-2000 23-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 20-CC
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RESULT 7
AAL04522/c
ID AAL04522 standard; DNA; 23934 BP
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                                                                                                                                                                                              The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (antjagonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rhemmatoid arthritis and ulcerative colitis; CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and CC parasitic infections.

CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly cx
                                                                                                                Query Match
Best Local S
Matches 18
                                                                 10877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
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05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                         Sequence 23934 BP; 7785 A; 4761 C; 4365 G; 7023
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
17-NOV-2000;
                                                                                        172 ctacaaattttgaaaata 189
                                                                2001-451937/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA,
                                                                                                                 l Similarity
18; Conserv
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                                                                                                                5.7%;
llarity 100.0%;
Conservative (
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2000US-0249216
2000US-0249218
2000US-0249244
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2000US-02511856
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2000US-02511899
2000US-0254097
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 2544; 781pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                10894
                                                                                                                 0;
                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS.
                                                                                                                          DB
22;
                                                                                                                                       22;
                                                                                                                 0;
                                                                                                                                                                           T; 0 other;
                                                                                                                                       Length 23934;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                0;
                                                                                                              Gaps
                                                                                                                0,
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18-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

01-SEP-2000

                                                                                                                                                                                                                                                                                                                                    14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL04522;
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Human reproductive system related antigen DNA SEQ ID NO:
                                       21-NOV-2001
                                     (first entry)
7210
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.

17-JAN-2001; 2001WO-US01339

18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 16-MAR-2000; 17-MAR-2000; 2000US-0179065
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English.

used

0;

Gaps

0

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2000US-0249210
2000US-0249211
    RESULT
AAS28343
ID AAS2
XX AAS2
XX AAS2
XX Geno
XX Huma
XW Lung
KW Iung
KW Iung
KW Iung
KW IOO
CS HOMC
XX WO2C
PN WO2C
PN WO2C
XX HOMC
AX HOMC
XX HOMC
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Best Local S
Matches 18
  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
11-MAR-2000;
18-PAR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                         02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence #183 encoding
                                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                  WO200155448-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS28343 standard; DNA; 23934 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ctacaaattttgaaaata 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23934 BP; 7023 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a reproductive is used in preventing, treating or ameliorating a medic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
2000US-0179065.

2000US-0180628.

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2000US-0188350.

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2000US-0199076.

2000US-0198123.

2000US-0298123.

2000US-0205515.

2000US-0209467.

2000US-02145135.

2000US-0216647.
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2000US-0251866.
2000US-0251869.
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0251997.
2000US-0251097.
2000US-0254097.
                                                                                                                                                                                                                                                                                           2001WO-US01333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 7210; 1297pp + Sequence Listing;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory antigen.
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25-SEP-2000
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29-SEP-2000
20-CCT-2000
20-CCT

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20-OCT 2000

20-OCT 2000

01-NOV 2000

08-NOV 2000

17-NOV 2000

17-NO
The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequence
                                                                                                                                                                                                             Isolated polypeptide disorders related to cancers and also for
                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                       ( HUMA - )
                                                                                                                                                                                                                                                                                      2001-476224/51.
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                                                                                                                                                                                                                                                                                                                                                                                          HUMAN GENOME
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2000US -02511989
2000US -0251989
2000US -0251989
                                                                                                                                                                              ID No
                                                                                                                                                                                                                                                                                                                        SC,
                                                                                                                                                                                                             for treating, preventing and/or prognosing the respiratory system including respiratory testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                           SCI
                                                                                                                                                                            777;
                                                                                                                                                                                                                                                                                                                        Ruben
                                                                                                                                                                            546pp; English
                                                                                                                                                                                                                                                                                                                        SM;
     polynucleotide sequences
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2000US-0241786

2000US-0233063. 2000US-0233064. 2000US-0233065. 2000US-0234274. 2000US-0234274. 2000US-0234997. 2000US-0234998.

2000US-0232398. 2000US-0232399. 2000US-0232400. 2000US-0232401.

2000US-0232081. 2000US-0231968. 2000US-0232397.

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RESULT 9
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AAK71442 Standard; D
XX
AC AAK71442;
XX
DE 06-NOV-2001 (first
DT 06-NOV-2001 (first
DT 06-NOV-2001) (first
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XX
DE Human immune/haemato
XX
DE Human; immune; haema
KW cytostatic; gene the
CS Homo sapiens.
XX
PN WO200157182-A2.
XX
PN WO20015-A2.
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PN WO2
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Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Local
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atic; gene therapy; vaccine; metastasis; ds.
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I Similarity 100.0%; 18; Conservative 0;
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       2000US-0179065.
2000US-0186658.
2000US-0184664.
2000US-0198123.
2000US-0198123.
2000US-0214886.
2000US-0214886.
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2000US-0216847.
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2000US-0224518.
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2000US-0225214.
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 13-OCT 2000
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                                                                                                                                                                                                                                                                                                            amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) comprehensially and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own product the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the complement (I) proteins and polynucleotides may be used to prevent, complement (I) proteins and polynucleotides may be used to prevent, concers and cancer metastases of haematopoietic-derived cells. AAK4703 concers and cancer metastases of haematopoietic-derived cells. AAK4703 concers and cancer metastases of haematopoietic actived cells. AAK4703 concers from the present invention. AAK54942 to AAK54950 and AAM82169 concers sequences used in the exemplification of the present invention.
                                                                                                                                           Query Match
Best Local Similarity
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05-DEC-2000;
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13058 CTACAAATTTTGAAAATA 13041
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                                                                                                                                                                                                                                                                    Sequence
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                        172 ctacaaattttgaaaata 189
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                                                                                                                                                                                                                                                                    23934 BP;
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                                                                                                                  Conservative
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2000US-0251869
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2000US-0249264.
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2000US-0249217.
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Pred. No.
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                                                                                                                  Mismatches
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22;
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RESULT 1
ANH92576
ID AAH92576
AC AAH9
XX AAH9
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XX Chr.
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RESULT 1
AAH04423
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Best Local Similarity 100
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                  Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 699 BP; 192 A; 142 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-367874/38
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10-APR-2000;
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                                                                                                                                                                                            26-JUN-2001
                                                                                                                                                                                                                                                   AAH04423;
                                                                                                                                                                                                                                                                                                      AAH04423 standard; cDNA; 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          372 aacaaatgaaatcagtt 388
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                                                                                                                                         CDNA
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                                                                                                                                      clone (5'-primer) SEQ ID
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2000US-0196046
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                                                                                detection; diagnosis; antisense therapy; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rioux J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                         NO:1258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
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70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 699;
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RESULT 1
AAZ36779
ID AAZ3
XX
AC AAZ3
XY
DT 13-M
XX
DE Nucl
XX
KW Huma
KW neur
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                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary CC to the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cC complementary to a complementary to 
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
       neurological
                                                           Nucleotide
                                                                                                  13-MAR-2000
                                                                                                                                                                    AAZ36779 standard;
                       Human; AHCP
                                                                                                                                     AAZ36779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                    175 caaattttgaaaataga 191
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 1258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000;
                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention.
                                                                                                                                                                                                                                                                caaattttgaaaataga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                             l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                      726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai
                                                           sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama
   gene; autosomal highly conserved protein;
l disease; genetic predisposition; chromoso
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0248036
99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                  252 A; 109
                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa
T, Wakama
                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                           5.4%;
                                                           the
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Wakamatsu
                                                                                                                                                                       842
                                                       human AHCP gene clone 3.
                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                           Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K,
A, Nagai I
                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                         DB
70
                                                                                                                                                                                                                                                                                                                                                                                                                                  Τ;
                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                               3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saito K, Y, Otsuki T;
chromosome 6p23; D6S274;
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                        Length 726
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 13
AAH94373/c
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                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                         nootropic; neuroprotective; thrombolytic; osteopathic; an gene therapy; antisense therapy; cancer; immune disorder; growth disorder; osteoporosis; thrombolytic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                       (autosomal highly conserved protein) gene. The AHCP gene is linked to a genetic predisposition to schizophrenia. The gene is located on chromosome 6p23, between markers D6S274 and D6S285. Several polymorphisms are found in the AHCP gene. Oligonucleotide probes derived from the AHCP sequences can be used to screen for patients having a genetic predisposition for a neurological or psychological disease, especially schizophrenia. The invention is used to diagnose a genetic predisposition to schizophrenia, and to treat the disorder by gene therapy. The invention provides a treatment that is specific to schizophrenic disorders, without the risk of significant side effects.
                               02-AUG-2001
                                                     WO200155339-A2
                                                                                                                                                                   Human
                                                                                                                                                                                        05-OCT-2001
                                                                                                                                                                                                               AAH94373;
                                                                                                                                                                                                                                   AAH94373 standard;
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ36777-84 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene encoding autosomal high conserved genetic predisposition to schizophrenia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1998;
31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leroy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D6S285; psychological disease; gene therapy;
                                                                                                                                                                                                                                                                                         283 gattttaagaaataact
                                                                                                                                                                                                                                                                                                     15 gattttaagaaataact
                                                                                                                                                                  foetal cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ρ,
                                                                                                                                         foetal protein; cytostatic;
                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conserv
                                                                                               system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INST PASTEUR.
INSERM INST N
                                                                                                                                                                                                                                                                                                                                                                                         842 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bourgeron T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 66-67; 76pp; English.
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                       (first entry)
                                                                                               disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0083625
98US-0114592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-IB00846
                                                                                                                                                                                                                                                                                                                                                                                         258 A;
                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                   cDNA;
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                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlapping clones
                                                                                                                                                                 ID NO:
                                                                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                         135
                                                                                                                                                                                                                                   1239
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                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                              Score 17;
Pred. No.
                                                                                                                                                                  902.
                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                         158 G;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                           immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                         291 T;
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                                                                                                                                                                                                                                                                                                                                           DB
70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the complete e. The AHCP gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                         0 other;
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                                                                                             sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jamain
                                                                                                                                           immunostimulant;
                                                                                                                               antiinflammatory;
                                                                                             tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnose
                                                                                                                                                                                                                                                                                                                                  0;
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25-JAN-2001; 2001WO-US02723.

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RESULT 1

ABA45382

ID ABA4

XX ABA4

AC ABA4

XX Huma

XX Huma

XX Huma

XX Huma

XX Homc

X
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Best Local
                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polynucleotides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present sequence is a full length cDNA which was assembled using expressed sequence tags (ESTs) found to be expressed in human foetal tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel fetal proteins useful for the treatment and diagnosis of diseases associated with dysfunction of the protein e.g. cancers, immune disorders, growth disorders, thrombolytic disorders, nervous system disorders and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeung Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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15-SEP-2000; 2000US-0663870
06-NOV-2000; 2000US-0707351
                                                                                                                                                                                                                                                                                                                                                                                         WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast cell single exon nucleic acid probe #4077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA45382 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1239 BP; 370 A; 187 C;
                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA45382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 tgagaaatagaacaaat 50
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  SG,
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)B; AAM06698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conserv
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                                             MOLECULAR DYNAMICS INC
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  Hanzel DK,
                                                                                                                ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                               2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyle
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA; 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%;
  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ, Arterburn MC, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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Best Local S
Matches 17
                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New spatially-addressable set of single exon nucleic acid puseful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 4077; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                            Penn SG,
                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                     WO200157277-A2
                                                                                                                                                                                                                                                                                                                                Human; foetal liver;
                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #4177.
                                                                                                                                                                                                                                                                                                                                                                                                                         ABA55872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA55872 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1959 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a spatially-addressable set of single
                                                        (MOLE-)
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                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                            Hanzel DK,
                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 A;
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                gene expression; single exon nucleic acid probe;
                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17;
Pred. No.
                             Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 531 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
71;
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WPI; 2001-483447/52

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ΩУ
Search completed: September 16, 2002, 06:31:41 Job time: 7649 sec
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                                                                                                                                                                                                                                                                                                    Query Match 5.4%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 71 Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4177; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1959 BP; 521 A; 343 C; 564 G; 531 T; 0 other;
                                                                                                                                                                  124 agttgtgttgcctttgt 140
|||||||||||||||||
|270 agttgtgttgcctttgt 286
                                                                                                                                                                                                                                                                                                                                        Score 17; DB 22; Length 1959; Pred. No. 71;
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Title: Perfect score: Sequence:

OM nucleic

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Scoring table:

Minimum DB Maximum DB

seq

Word size

Searched:

sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence

1, Appli 176, App 176, App 176, App 4, Appli 4, Appli 4, Appli 1, Appli 1, Appli 5, Appli 5, Appli 5, Appli 1, Appli 1, Appli 1, Appli 1, Appli 5, Appli

Sequence

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Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed
is derived by analysis of the total score distribution.
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length: 2000000000
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Match Length
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315
1 tamacactgactcagatttt.....tgtgtattatctacttatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLIGO_NUC Gapop 60.0 , Gapext 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383533 seqs, 122816752 residues
   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
   /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
 DB
               US-08-952-127-11
US-08-951-822A-15
PCT-US95-0774A-15
US-08-991-789A-264
US-09-962-451-264
US-09-966-713-1
US-08-916-857-1
US-08-96-713-1
US-08-96-713-1
US-08-96-95-54-64
US-08-452-654-64
US-08-452-654-64
US-08-452-654-64
US-08-452-654-64
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US-08-452-654-64
US-08-452-654-64
US-08-452-654-64
US-08-452-658-64
US-08-350-260A-266
US-08-350-260A-266
US-08-350-260A-267
US-08-86-164-19
US-08-86-164-19
US-08-86-164-19
US-08-86-164-19
US-08-896-164-19
US-08-896-164-19
US-08-896-164-715-15
US-09-296-715-15
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sequence
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             15, Appl
264, App
264, Appl
264, Appli
1, Appli
27, Appli
64, Appl
65, Appl
66, Appl
66, Appl
67, Appl
68, Appl
69, Appl
60, Appl
60, Appl
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60, Appl
61, Appl
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US-08-952-127-11
Sequence 11, Application
Patent No. 6211336
Patent No. 6211316
GENERAL INFORMATION:
                                                                           ; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome
US-08-952-127-11
                                                                                                                                                                   APPLICATION NUMBER: US/08/952,
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KOhn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5055
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTECHIE TYPE: COLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6211336thwestern Hwy., Suite .
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
APPLICANT: COLLINS, FRANCIS S.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08952127
 Conservative
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1569
1569
1734
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11734
11886
1886
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1886
5.7%; Score 18; DB
100.0%; Pred. No. 2.
tive 0; Mismatches
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US-09-273-142-1
US-08-743-637B-176
US-08-743-637B-176
US-08-551-437-4
US-09-004-225-4
US-09-104-704-4
US-09-104-704-4
US-09-104-704-4
US-08-659-939-1
US-08-659-939-1
US-08-850-041-1
US-08-858-1940-5
US-08-858-344D-5
US-08-976-397-1
US-08-976-397-1
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                              Length 9620;
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Result No.

Score

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Gaps

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RESULT 3
PCT-US95-07744A-15
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US-08-261-822A-15
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                                                                                                                                                                                        Sequence 15, Application PC/TUS9507744A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 4146 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
DEGITEDEMETON MINISTERS. 24.003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Ecker,
                                                                                      APPLICANT: Trustees of The Universities of Invention: Plant Genes for Invention: and Pathogens NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             1284 AAATTTTGAAAATAGAT 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NATI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               176 aaattttgaaaatagat 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6071 TCTCTTAGAGATCTACAG 6088
                                               STREET: One Liberty CITY: Philadelphia
   ZIP:
                                     STATE:
                                                           ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris STREET: One Liberty Place, 46th floor
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 19103
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o. 5650553
19103
                                  PΑ
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                  USA
                                                                                                                                              Trustees of The University of Pennsylvania VENTION: Plant Genes for Sensitivity to Et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 1; Pred. No. 7.7;
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                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                               Length 4146;
                                                                                                                                                  to Ethylene
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RESULT 4
US-08-991-789A-264/c
Sequence 264, Application US/08991789A
Patent No. 6225054
GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: 08/261
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
       ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/991,789A

FILING DATE: 11-Dec-1997

CLASSIFICATION : CUnknown>
ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION UNBER: 210121.419C3

TELECOMMUNICATION INFORMATION:

TETERDOMMUNICATION INFORMATION:

TETERDOMMUNICATION INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 aaattttgaaaatagat 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Frudakis, Tony N.
TELEPHONE:
                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        STATE: Washington
                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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Reed, Steven G.
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100.0%; Pred. No. 7.
ative 0; Mismatches
(206)
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-991-789A-264
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Best Local Similarity
Watches 16; Conserve
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US-08-616-857-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 264, Application US/09062451
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/062
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 715 base pairs
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                                                                                                                                                                                                                                     715 base pairs
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ilarity 100.0%;
Conservative
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Of Columbia Center,
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Pred. No.
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Pred. No.
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; NAME/KEY:
; LOCATION:
US-08-616-857-1
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US-08-906-713-1
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GENERAL INFORMATION:
APPLICANT: Lecka-
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Best Local 9
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: Zymogenet
                                                                                                                                                    APPLICANT: Jelmberg, Anna C.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Farrah, Theresa M.
TITLE OF INVENTION: MAMMALIAN ZC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Freeman, John F. REGISTRATION NUMBER: 29,066 TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: NOVEL DNA BINDING PROTEIN S1-3
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                                                                                                                                                                                                                                                                                                                                                                            180 tttgaaaatagattgt 195
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STRANDEDNESS: single
TOPOLOGY: linear
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                                           COUNTRY:
                                                                                          STREET:
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                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street
                              ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                          E: Zymogenetics
1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1161 base pairs
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                                                                                                                                                                                                                               Lok, Si
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Pred. No.
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25;
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COMPUTER:

IBM Compatible

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-381-862-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Applic Patent No. 6245906
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                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keshi, Hiroyuki
APPLICANT: Matsuhisa, Akio
TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS
TITLE OF INVENTION: CAUSED BY STREPTOCOCCUS PYOGENES
               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ueyama, Hiroshi
APPLICANT: Abe, Kanako
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2631 AACAAATGAAATCAGT 2646
                                                                                                                                                                                                                                                              STREET: 20.
CTTY: Chicago
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REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 aacaaatgaaatcagt 59
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                                FILING DATE:
                                                                                  CLASSIFICATION:
                                                                                                   FILING DATE:
                                                                                                               APPLICATION NUMBER:
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Local Similarity 100.0%;
nes 16; Conservative 0;
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233 South Wacker Drive/6300 Sears Tower
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PCT/JP98/01288
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Query Match
Best Local Similarity
"~+~hes 16; Conserv:
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US-09-381-862-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2
Patent No.
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312) 474-044 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              FILING DATE: 04-NOV-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                               FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5369 AAATAACTTTTGAGAA 5354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                             NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
                                                TELEPHONE:
                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: MILWAUKEE
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 aaataacttttgagaa 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus pyogenes
STRAIN: Clinical Isolate SP-26-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 19036/36274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cawley, Jr., Thomas A. REGISTRATION NUMBER: 40,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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40. 5994066
                                                                                                                                                                                                                                                                                                                                                    53202-4497
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                                                                                                                                                                                                                                                                                                                                                                                   WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08743637B
               (414) 277-5000
(414)277-5591
OR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                 E: QUARLES & BRADY
411 EAST WISCONSIN AVENUE
                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BERGERON, Michel G. PICARD, Francois J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROY, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OUELLETTE, Marc
                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                 04-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-1998
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474-0448
MO: 5:
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
                                                                                                                                                                US 08/526,840
                                                                                                                                                                                                                               US/08/743,637B
                                                                                 850586.90012
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US-08-526-840B-27
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Query Match
Best Local Similarity
Watches 16; Conserve
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                                                                                                                                                                                                                                ATTORNEY/AGENT INFO....
ATTORNEY/AGENT LIFE....
NAME: BAKER, Jean C.
NAME: BAKER, Jean C.
REFERENCE/DOCKET NUMBER: 85058
TELECOMMUNICATION INFORMATION:
TELECHONE: (414) 277-5900
TELECHONE: (414) 277-591
TO NO: 27:
                                                                                                                                                                                                                                        TELEFAX: (414) 277-559
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOOLGGY: linear
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APPLICANT:
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ORIGINAL SOURCE:
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/304,732 FILING DATE: 12-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Milwaukee
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OUELLETTE, Marc
             5.1%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                            Haemophilus influenzae
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                                                                                                                                          DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
177
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                       850586.90012
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             Mismatches
                             DB 3;
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              0;
                                            Length 9100;
              Indels
              0;
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           Gaps
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RESULT 11
US-07-741-940-64
                                                          RESULT 12
US-08-289-548A-64
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Sequence 64, Application US/08289548A Patent No. 5648212
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
                                                                                                                                                                                     Matches
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                           199 acaataaactggagt 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: U: FILING DATE: 19920109 CLASSIFICATION: 435
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                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                         1 ACAATAAACTGGAGT
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5. 5352775
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                                                                                                                                                                                     l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                   23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Banner, Birch, 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANAND, RAKESH
CARLSON, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALBERTSEN,
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                    4.8%; Score 15; DB
100.0%; Pred. No. 84
tive 0; Mismatches
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                                                                                                                                                                                                  DB 1;
. 84;
                                                                                                                                                                                     0,
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US-08-452-654-64
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                                                                                                                                                                                                              Sequence 64, Applicat
Patent No. 5691454
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                     APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: KINZLER, KENNETH
APPLICANT: MAKKHAM, ALEXANDER
APPLICANT: MAKKHAM, ALEXANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
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NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/289,548A FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1001 G St
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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20001-4598
T: THLIVERIS, ANDREW
INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.C.
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linear
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GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                       KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
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100.0%; Pred. No.
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Best Local Similarity
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INFORMATION FOR SEQ
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR TON NUMBER: US 07/741,940
APPLICATION NUMBER: 08-AUG-1991
APPLICATION OB-AUG-1991
                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                             TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
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CORRESPONDENCE ADDRESS:
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COUNTRY: USA
ZIP: 20001-4598
                                STATE:
                                            CITY: Washington
                                                           STREET:
                                                                             ADDRESSEE: Banner & Witcoff, Ltd
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                                                           1001 G Street, NW
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1001 G Street, NW
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THLIVERIS, ANDREW
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HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                                                                                                                                             KINZLER, KENNETH MARKHAM, ALEXANDER F.
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100.0%; Pred. No.
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CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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Best Local Similarity
Matches 15; Conserv
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           TITLE OF INVENTION: INHERITED AND SUMMALIC MULTALICAL CANCER IN HUMANS TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS NUMBER OF SEQUENCES: 102
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ORIGINAL SOURCE:
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LENGTH: 23 base pairs
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APPLICATION NUMBER:
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                                                                          COUNTRY: USA
ZIP: 20001-4598
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                             STATE:
                                                                                                                       STREET: 1001 G St
CITY: Washington
                                                                                                                                          ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, NW
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HEDGE, PHILIP J.
JOSLYN, GEOFF
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THLIVERIS, ANDREW
ENTION: INHERITED AND SOMATIC MUTATIONS OF APC
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ANAND, RAKESH
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PatentIn Release #1.0, Version #1.25
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7 100.0%; Pr
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Pred. No.
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Search completed: September 16, 2002, 06:24:21 Job time: 10634 sec
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Best Local Similarity
Matches 15; Conserv
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PRIOR APPLICATION NUMBER: US 07/741,940

FILING DATE: 08-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-508-919
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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PRIOR APPLICATION DATA:
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                                                                                                  199 acaataaactggagt 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                 1 ACAATAAACTGGAGT
                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                               Conservative
                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                         100.0%; F1
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                                                                                                                                                               Score 15;
Pred. No.
                                                                                                                                              Mismatches
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84;
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Gaps

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Title:
Perfect score:
Sequence:
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length: 2000000000
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                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RCl&t2=RCl-CT0469-
160800-011-e04&t3=2000-08-16&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                    Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J. Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Marck EST Project
                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                Tel:
                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                  yv22a12.rl Soares fetal liver spleen IMAGE:243454 5', mRNA sequence.
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/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
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            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scriipts/gethtml2.pl?tl=RC3&t2=RC3-CT0283-201199-011-f12&t3=1999-11-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 262.
                                                                                                                                                                                                                                                                                                                                           Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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RC3-CT0283-201199-011-f12
AW753759
AW753759.1 GI:7668691
EST.
                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                    Brazil
                                                                                                                                                                                                                                                                                                  sequence tags
                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                    Simpson, A.J
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Mammalia; Eutheria;
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Location/Qualifiers
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/db_xref="GDB:3792587"
/db_xref="taxon:9606"
/clone="MAGE:243454"
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Primates;
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CT0283 Homo sapiens cDNA,
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1.6e-30;
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                                                                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 252 row: C column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Feat: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-252C22.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao, S., Nierman, W., Malek, J., Shatsman, S., A. Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Russell, D., de Jong, P. and Fraser, C.M.
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RPCI-24-252C22.TJ RPCI-24
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
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/cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-252C22"
                                                                                                                                                        /clone_lib="RPCI-24"
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/clone_lib="CT0283"
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/organism="Homo sapiens"
                                                                                                                                    /sex="Male"
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Pred. No.
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s musculus genomic clone RPCI-24-252C22
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1e-10;
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Best Local
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                                                                                                                                 112 acatacaaagtcagttgtgtt 132
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                                                                                                                ACATACAAAGTCAGTTGTGTT 46
                                                                                                                                                                               21;
AZ319774 578 bp DN 1M0039F04R Mouse 10kb plasmid UUGC1M clone UUGC1M0039F04 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 3138 row: P column: 11
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatiful; (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 685)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ780202 685 bp DNA linear GSS 02-AUG-1999 HS_3138_B1_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138 Col=11 Row=P, DNA sequence. AQ780202 AQ780202.1 GI:5683162
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                                                                                                                                                                             6.7%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (206) 616-3887
L: jwallace@u.washington.edu
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E-Coli DH10B"
132 c 94 g 174 t 1 others
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3138 Col=11 Row=P"
/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                                                                                                                                                                                                                                                            /sex≃"male"
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Pred. No.
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Pred. No.
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                                                                                                                                       63 TAGAAGGAAATACAACATTC
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AV163511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0039 row: F column: 04
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                   Similarity
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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AZ319774.1
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-comptent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid ends
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Mus musculus head C57BL/6J 13-day
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector:
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0039F04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No.
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  Mus musculus cDNA
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                                                                                               AUTHORS
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nes 19; Conserv
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Muramatsu, M., Una
Mouse ESTS
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1 (bases 1 to 258)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvelho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                   PMO-HT0913-250401-015-C04 HT0913 Homo sapiens cDNA, BG999039
                                                                                                                                             Mammalia;
                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                             BG999039.1 GI:14403111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998)) Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Conservative
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/dev_stage="13-day embryo"
31 c 37 g 73 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3110011B18"
                                                                                                                                             Eutheria;
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Primates; Catarrhini; Hominidae;
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nes 19; Conser
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                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                   C56866 C56866.1 GI:2414897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-HT0913-
250401-015-C04&tj=2001-04-25&t4=1)
                                                                         Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                               Kohara,Y., Motohashi,T., Tabara,H.,
,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 22 High quality sequence stop: 258.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                    Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1..300
                                                                                                                                                                            Contact: Yuji Kohara
                                                                                                                                                                                            Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue mRNA and cDNA amplification were performed under low stringency conditions."

53 c 55 g 65 t
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/clone_lib="HT0913"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/organism="Caenorhabditis elegans"
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 TGACTACAAATTTTGAAAA 361
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                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COW.
                                                                                                                                                                                                                                                                                                                                                                     Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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                                                                                                                                                                                                                                                                                                                                        Email: smoore@afns.ualberta.ca
Insert Length: 364 Std Error:
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a 69
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/clone_lib="Yuji Kohara unpublished cDNA"
/clone_lib="Yuji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
29 c 59 g 70 t 4 others
                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bos taurus Duodenum #1 library"
/tissue_type="Smooth muscle"
/tell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XL1_BlueMRF'strain"
                                                                                                                                             /note="Organ: Intestine/duodenum;
Site_1: EcoRI; Site_2: Xho I"
69 c 62 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Sus scrofa
                                                                                  AQ669043 416 bp DNA linear GSS 24-JUN-
HS_5414_A2_A09_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=990 Col=18 Row=A, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dT track served to verify it as a clone from the non-normalized anterior pituitary at estrus day 0 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science will be of Missouri-Columbia, 65211 Clone distribution: clones will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 376)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                            AQ669043
AQ669043.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cktuggle@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 5152944252
Fax: 5152942401
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201 Kildee Hall, Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Genetics Laboratory, Department of Animal Science
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TAG_SEQ=TAAGGC"

1 65 c 57 g 121 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_LIB=MI-P-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9823"
/clone="MI-P-A1-acm-g-11-1-UM"
/clone_lib="MI-P-A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="crossbreed"
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Sus.
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Class: BAC ends
                                                                                                                     Kitayama,A.,
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280 tcaggataatttgtcatgt 298
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BJ075543 GI:17520459 EST.
African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
Contact: Tadasu Shin-i
                                                                                                                              Amphibia; Batrachia; Anura; Mesobatrachia; Xenopodinae; Xenopus.

1 (bases 1 to 510)
                                                                                                                                                                                                     Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.htsc.washington.edu
Plate: 990 row: A column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                          Unpublished (2001)
                                                  Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 416.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jwallace@u.washington.edu
                                                                                                 (bases 1 to 510)
ayama,A., Terasaka,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

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/clone_lib="RPCI-11 Human Male I
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/db_xref="taxon:9606"
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Tel: 301-838-3523
Fax: 301-838-0208
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19; Conser
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Other_GSSs: BOGXT64TR
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 585)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOGXT64TF BOGX Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                          Class: sheared ends
                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                         Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
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Fax: 81-559-81-6855
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llarity 100.0%;
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/db_xref="taxon:8355"
/clone="XL057o04"
                                                                                                              /clone_lib="BOGX"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
116 c 110 g 171 t
                                                                                                                                                                     /organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGXT64"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole embryo"
/dev_stage="stage 25"
107 c 110 g 137 t
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tawaka,T., Matsuura
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jappel: 81-45-503-9222 Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                   /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="0H10B"
/note="Site_1: Sall; Site_2: B
                                                                                                                                                                                                          spinal ganglion"
                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Search completed: September 16, 2002, 05:18:16 Job time: 8389 sec
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ORIGIN
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/Backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-022-409-85
US-08-680-726A-86
US-09-032-409-85
US-09-032-409-86
US-09-032-409-86
US-09-033-13-535
US-08-906-769-142
US-08-906-769-142
US-08-906-613-142
US-09-012-692-142
US-08-906-613-142
US-08-906-613-142
US-08-916-13-142
US-08-918-136-27
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US-08-920-812-2
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US-08-917-913-11
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APPLICANT:
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APPLICANT:
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                     MOLECULE TYPE:
                                 LENGTH: 9919 base partype: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 10591
                                                                                                                                                                                                                                                                                                   CITY: Tarrytown
STATE: New York
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Friedrich, Leslie
Weymann, Kristianna
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Sequence 1, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 59, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 17, Appl		•	Sequence 14, Appl	Sequence 13, Appl	Sequence 12, Appl

ALIGNMENTS

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APPLICANT: Weymain, ALISTIANIA
APPLICANT: Ellis, Daniel
APPLICANT: Uses, Taco
APPLICANT: Uses, Taco
APPLICANT: Uses, Taco
APPLICANT: Uses, Pieter
TITLE OF INVENTION: SIGNL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED
TITLE OF INVENTION: SIGNL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED
TITLE OF INVENTION: SIGNL TRANSDUCTION CASCADE LEADING TO SYSTEMIC ACQUIRED
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 17
CORRESSE: NO. 6091004artis Corporation
ADDRESSEE: NO. 6091004artis Corporation
STRET: SOU White Plains Road, P.O. Box 2005
CITY: Tarrytown
STRET: SOU White Plains Road, P.O. Box 2005
CITY: Tarrytown
STRET: New York
COUNTRY: USA
ZIF: 10591
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/880,179
FILING DATE:
APPLICANTION STATE
APPLICANTION STATE
NAME: Meigs, J. Timothy
REGISTRATION UNMBER: US/08/880,179
FILEDHOME: (919) 541-8689
TELECOMMUNICATION INFORMATION:
TELEPHOME: (919) 541-8689
INFORMATION FOR SED ID NO: 1:
SOUDENCE CHARACTERISTICS:
LENGTH: 9919 base pairs
TRANSDENCES: single
TOPOLOGY: Ilnear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
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US-08-880-179-1

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                     Query Match
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Best Local
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                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
                                                                                                                                  FEATURE:
                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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APPLICANT: Frank, Rexann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                      NAME: Connell, Gary J. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/680,726A FILING DATE: 12-JUL-1996 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Street, Suite 3500
    0;
                     Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                       2618-46-C1
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    Mismatches
                                 DB 1;
   65;
                                 Length 747;
   Indels
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US-09-092-409-87
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                                                                                                                       Query Match
Best Local Similarity 51.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 87, Application US/09092409 Patent No. 6159478
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-JUL-196
ATTORNEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 863-02 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haanes, Elizal APPLICANT: Frank, Rexann
                                                                                    174 acaaattttgaaaatagattgtcacacaataaactggagtttatggaaacatcagtagaa 233
                   234 ggaaatacaacattccattccctttacagagatcatttacttgcaactccaggataatttgt 293
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80 CAAAATTAATACTTTCTTGTATTGATGATCAGCATACGTTTAATATTCATGATGATTTAA 139
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                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Sheridan KUSS & FRANCES STREET: 1700 Lincoln Street, Suite 3500
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                                                                  AAAATAATTATGAAGCGTCTGTTATAGCTAAATCTTTATTATATGGAAACCCAATCTCTA 79
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                                                                                                                                                                                                                                                                                                                                                           747 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                              863-0223
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51.9%;
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                                                                                                                                    Score 31; DB 3; Pred. No. 3.3; 0; Mismatches 6
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                                                                                                                                    65;
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                                                                              Sequence 86, Application US/08680726A Patent No. 5804197
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                                                                  GENERAL INFORMATION:
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FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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               APPLICANT: Haanes, Elizabeth J. APPLICANT: Frank, Rexann S. TITLE OF INVENTION: RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                  610 TAACTATATTATCTA 596
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OPERATING SYSTEM:
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COMPUTER: IBM PC compatible
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12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                   9.8%;
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               RECOMBINANT CANINE HERPESVIRUSES
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Pred. No.
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; TOPOLOGY: 1:
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US-08-680-726A-86
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                                                                                                                                                                                                                                                                                                                           Sequence 85, Application US/09092409 Patent No. 6159478
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                               APPLICANT: Haanes, Elizabet
APPLICANT: Frank, Rexann S
TITLE OF INVENTION: RECOMB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700 TELEFAX: (303) 863-0223
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CURRENT APPLICATION DATA:
                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MEDIUM TYPE: Floppy disk
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               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 acaaattttgaaaatagattgtcacacaataaactggagtttatggaaacatcagtagaa 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  STREET: 1700
CITY: Denver
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                                                                                                                                     COUNTRY:
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APPLICATION NUMBER:
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                                                                                                                                    U.S.A.
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                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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                                                                                                                                                                                                                                                                                        Elizabeth J.
                                                                                                                                                                                                                                                        RECOMBINANT CANINE HERPESVIRUSES
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                                                                                                                                                                                                                                        92
US/09/092,409
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Pred. No.
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US-09-092-409-86

; Sequence 86, Application US/09092409

; Patent No. 6159478
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           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,(
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haanes, Elizab
APPLICANT: Frank, Rexann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Denver
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                 APPLICATION NUMBER: US/09/092,409
                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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TELEPHONE:
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%;
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NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535
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Best Local Similarity 51.9
                                                                                                                Query Match
Best Local Similarity
Matches 42; Conserv
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APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: RESOURCE CHARACTERISTICS:
LENGTH: 749 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
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4327 T 4327
                                                             MOLECULE TYPE: DNA (genomic)
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                                                                             3 aacactgactcagattttaagaaataactttttgagaaatagaacaaatgaaatcagtttc 62
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5. 6329505
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Retter, Mark
Solk, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harlocker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitcham, Jennifer L.
                                                                                                                           Conservative
                                                                                                                                         9.7%;
68.9%;
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51.9%;
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                                                                                                                                          Score 30.6; DB 4; Length 6082; Pred. No. 8.3;
                                                                                                                           Mismatches
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RESULT 9 US-08-906-769-142/c

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RESULT 10
US-08-906-616-142/c
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Best Local
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TRICFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gaines, P
APPLICANT: Silver, G
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCYDOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 01 FILING DATE: 24-APR-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..384
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                      280
                                                                                                                                                                                                                     139
                                                                                                                          220
                                                                                                                                                         199
                                                              160 CAGGTTTGATAGATTTTGAGTTAAAAACAATTTTT 126
                                                                                                                                                                                                                                                  Local Similarity 
les 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                               cagagatcatttacttgcaactcaggataatttgt 293
                                                                                                                         AACCTGCCACGGTTGCTATTGAACCATTAGCCGTTTCGATTCCTTCATCAATTAGCTTTA 161
                                                                                                                                          acaataaactggagtttatggaaacatcagtagaaggaaatacaacattccatcccttta 258
                                                                                                                                                                                    GTACATTTACAGCCAATAAATAATTAGGTATGTACGGAAAACCATCCACTACTTTACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu Hunter, Shirley
                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rushlow, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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303) 863-0223
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MOLECULES AND USES THEREOF
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Pred. No. 4.6;
0; Mismatches
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RESULT 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (303) 863-022.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                /note- "At pos. bp 3, change A to R."
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Pred. No. 4.6;
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Sequence 142, Application US/08639075A Patent No. 6150125

APPLICANT: Grieve

Grieve, Robert B.

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RESULT 12
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                                                                Sequence 142, Application US/09012431 Patent No. 6180383 GENERAL INFORMATION:
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Best Local
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NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE_POCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
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APPLICANT:
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TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                               139
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OTHER INFORMATION:
OTHER INFORMATION:
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FILING DATE: 24-APR-1996
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                              APPLICANT: Grieve, Robert B.
Rushlow, Keith E.
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Wu Hunter, Shirley Frank, Glenn R.
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US-09-012-692-142/c

; Sequence 142, Application US/09012692

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GENERAL INFORMATION:
APPLICANT: Grieve,
APPLICANT: Rushlow
APPLICANT: Wu Hunt
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Best Local Similarity 49.7%;
Matches 77; Conservative
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TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                              acaataaactggagtttatggaaacatcagtagaaggaaatacaaccattccatcccttta 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sheridan Ross & McIntosh STREET: 1700 Lincoln Street, Suite CITY: Denver
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LOCATION: 1..384
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               Grieve, Robert B.
Rushlow, Keith E.
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Silver, Gary
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863-0223
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Pred. No. 4.6;
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Rushlow, Keith Wu Hunter, Shi

APPLICANT:

Frank, Glenn

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                                           Sequence 142, Application US/08906613 Patent No. 6232096 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 08/639,075
APPLICATION UNMBER: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 386 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC TITLE OF INVENTION: MOLECULES AND USES THEREOF NUMBER OF SEQUENCES: 190
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                           160 CAGGTTTGATAGATTTTGAGTTAAAAACAATTTTT 126
                                                                                                                                                                            259 cagagatcatttacttgcaactcaggataatttgt 293
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                                                                                                                                                                                                                                                                                      280 GTACATTTACAGCCAATAAATAATTAGGTATGTACGGAAAACCATCCACTACTTTACCCC
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CITY: Denver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..384
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 1...
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Stiegler, Gary
              Grieve, Robert B. Rushlow, Keith E.
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 Wu Hunter,
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Pred. No. 4.
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RESULT 15
US-08-480-604A-27/c
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Sequence 27, Application US/08480604A Patent No. 5736139
GENERAL INFORMATION:
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NAME: CONDELL, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 24-APR-1996
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CORRESPONDENCE ADDRESS:
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STREET: 1,
OTTY: Denver
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LOCATION: 1.384
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 386 base pairs TYPE: nucleic acid STRANDEDNESS; single
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1700 Lincoln Street, Suite
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SYSTEM: PC-DOS/MS-DOS
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KINK, JOHN A.
THALLEY, BRUCE S.
PADHYE, NISHA V.

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US-08-480-604A-27
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MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION UMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION UMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: US-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/329,154
FILING DATE: US-CCT-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/329,154
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/985,321
FILING DATE: 03-DCT-1989
APPLICATION UMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: TRIGOLAR F
                                                                                                                                                                                                                                                        Query Match 9.5%;
Best Local Similarity 48.8%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                         2632 TAGAAGTATTAATAATATTCTTAATATATTCAGTAAATGTAGATAATAATCTTTGATTAT 2573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONIGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
224 atcagtagaaggaaatacaacattccattccctttacagagatcatt 269
                                                                                                164 aggtatgactacaaattttgaaaatagattgtcacacaataaactggagtttatggaaac 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPHD-01763
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Db 2572 CTACGTATTTGGAAAGCTGAAAAGGTATATCTGTACTAAGTGTATT 2527

Search completed: September 16, 2002, 03:26:45 Job time: 9328 sec

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Maximum DB seg length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AL069961 Drosophil
AL099388 Drosophil
AL075293 Drosophil
BF295719 027pbE02
AL106628 Drosophil
BF295718 AL639578
       BF572670 602079265
BI30054 384881 MA
BE231792 601084794
AW746159 WS1_39_D0
AL166171 Drosophi1
BH421278 BOHCQ62TR
AZ784456 2M0027G22
                                                                                                                                                                                    Description
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ALIGNMENTS

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-RCl&t2-RCl-CT0469160800-011-e04&t3-2000-08-16&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 559. Contact: Simpson A.J.G.
Laboratory of Cancer Cenetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and BF335657 563 bp mRNA linear RC1-CT0469-160800-011-e04 CT0469 Homo sapiens cDNA, BF335657 Tel: +55-11-2704922 Fax: +55-11-2707001 sequence tags Shotgun sequencing of the human transcriptome with ORF expressed Simpson, A.J. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens BF335657.1 GI:11306405 Natl. Acad. Sci. U.S.A. /organism="Homo sapiens" Location/Qualifiers 1 to 563) 97 (7), 3491-3496 (2000) mRNA sequence.

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KEYWORDS
SOURCE
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                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebr Mammalia; Eutheria; Primates; Catarrhini; Homin 1 (bases 1 to 513)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., M., Hultman,M., Kucaba,T., Le,M., Lennon,G., P. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trev,R., Williamson,A., Wohldmann,P. and Wilson,R. The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                 yv22a12.rl Soares fetal liver sp
IMAGE:243454 5', mRNA sequence.
N49446
                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 EST
                              Seq primer: T7
                                                                                                                                                                 Contact: Wilson RK
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone_lib="CT0469"
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99.7%;
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Pred. No. 2e
                                                                                                                                                                                                                             T., Le,M., Lennon,G., Marra,M., Parsons,J. Soares,M., Tan,F., Trevaskis,E., Waterston
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                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 323)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                    AW753759
RC3-CT0283-201199-011-f12
AW753759
AW753759.1 GI:7668691
                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                            Simpson, A.J.
Email: asimpson@ludwig.org.br
                                                                 Ludwig Institute for Cancer
                                                                                                                    Proc. Natl. Acad.
                                                                                                                                  sequence tags
                                                                                                                                                                                                                                                                             Homo sapiens
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                                                    Prof. Antonio Prudente 109,
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                           +55-11-2704922
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102 c 89 g 162 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:3792587"
/db_xref="taxon:9606"
/clone="IMAGE:243454"
/clone_lib="Soares fetal liver spleen lNFLS"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome
BACR27K04 of RPCI-98 library fr
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 844)
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High quality sequence stop: 262
Location/Qualifiers
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Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                      - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome sur BACN03B09 of DrosBAC library from
                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR27K04"
                                                                                        /organism="Drosophila
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                   /note="end : SP6"
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                                                       /clone="BACN03B09"
                                                                            /clone_lib="DrosBAC"
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                                                                                                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.speace.com/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosophila/prosop
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYMTATAHTATMTATMTAYAHWMTAYMYYMYYACTATAYTAYATATMTATMYTYTTTTTT 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Mnscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSU0DT7 1101 bp DNA linear GSS 04-JUN-19
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR28J21 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                     http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                               /clone_lib="RPCI-98"
/clone="BACR28J21"
                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                              Location/Qualifiers
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                            224 others
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Thes 79; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgaaaatagattgtcacacaataaactggagtttat 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 652)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence
Parasitol. Today 16 (10), 409 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Pathobiology, College of Veterinary Medicine University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainseville, FL 32611-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF295719
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027PbE02 Pb cDNA #17,
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352 392 9704
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                                                                                                                                                                                                                                                                                                                                                                                                                                    damej@mail.vetmed.ufl.edu
        the cDNA, and fragments were ligated into EcoRI/XhoI digested vector."

1 75 c 79 g 206 t 3 others
                                                                                               cell contamination estimated to be approximately 5%. PolyA+ RNA was extracted and reverse transcribed usioning of T-XhoI primer (Lambda ZAP II cDNA cloning kit,
                                                                                                                                                   /note="Vector: pBluescript II vector DNA, excised from Lamda ZAP II; Site_1: EcoRT; Site_2: XhoI; Total RNA was extracted from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei, grown in Wistar rats to 30% parasitemia and 2-5% gametocytemia. Contaminating host white cells had previously been removed and final host
                                                                                Stratagene).
                                                                    manufacturer's
                                                                                                                                                                                                                                                                                           Clara Frontali"
                                                                                                                                                                                                                                                                                                        /strain="ANKA clone HP (gametocyte producer)"
/db_xref="taxon:5821"
/clone_lib="Pb cDNA #17, Tommaso Pace, Marta
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                         /lab_host="Wistar rats"
                                                                                                                                                                                                                                                                        /dev_stage="asynchronous blood
                                                                                                                                                                                                                                                                                                                                                                /organism="Plasmodium berghei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:13946032
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36.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tommaso Pace, Marta
DNA 5', mRNA sequence
                                                                                  Second strand cDNA was made following the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 8
                                                                    protocol. EcoRI adaptors were ligated
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8.6;
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                                                                                                                                                                                                                                                                                                             Marta Ponzi,
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                                                                                                                       AWATCTTTTYCCCTCCCMYCCCMMCMMTTTYTTCCTMMMHWMMTTHMHTTMTTMHMMM 867
                                                                                                                                                                                                                                              ТТҮТТМТААТТНМСҮТНМТТТҮАММТММТСТМАТWАЛАММААААМТНСТМАМААНАМТWA 807
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ТТНИТТМИНТТНИМИНМИТТТМИНТТМНТНТТW-ТННМИТМИМТТНМИМИТТТМТ 926
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1204)
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/note="end : T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
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a 112 c 112 g 209 t 1 others
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/clone="TNAMA"
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/lab_host="Escherichia coli DH10B"
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75; Conser
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Plate: LLCM1080 row: b column: 18
High quality sequence stop: 326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF572670.1 GI:11646382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAAAGGCGAGCGGCGACATC-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

62 a 152 c 199 g 105 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:4253489"
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1 to 718)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109;
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases cal v0.980904.e. Vector identified by and minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 404 704 705 705 Fax: 404 705 Fax: 40
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Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 463)
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Fax: 402 762 4390
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Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                  EST
                                                                                                                                                                                            mRNA sequence.
BE291792
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/tlab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI;
/inote="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI;
/tibrary made from pooled tissue from testis, ovary,
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 42 c 85 g 160 t
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
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Rodentia;
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Pred. No. 16;
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                                                                                                                                                                                                                                                                    bp mRNA linear EST 13-JUL-2000 musculus cDNA clone IMAGE:3499150 5',
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                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                         WS1_39_D05.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLMA0555 row: k column: 23 High quality sequence stop: 564. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                            sorghum.
Sorghum bicolor
               Department of Botany
The University of Georgia
                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                              AW746159.1
EST.
                                               Contact: Cordonnier-Pratt MM
                                                                                                             Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                               AW746159
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                                                                 Unpublished (2000)
                                                                              An EST database from Sorghum:
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Clone distribution: MGC clone distribution information can
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/clone_lib="NOT_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
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/db_xref="taxon:10090"
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                                                               pBeloBAC11.
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528 AAACTAGTAAAAGTAATTGGCTTACATCAAACTGGAGCTTGAGCAATGTACAAATCAGGG
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                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL106171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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Direct Submission
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/note="organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
a 107 c 125 g 175 t
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/db_xref="taxon:4558"
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/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
                                                                                  Location/Qualifiers
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Pred. No. 21;
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                                                                                                                                                                       Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                             Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSSs: BOHCO62TF
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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Brassica oleracea
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                                                                                                                                                                                                                                                                                                Contact: Chris Town
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BH421278
                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid
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                   213
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/clone_lib="prosBaC"
/clone="BACN15C18"
/note="end: SP6"
a 128 c 38 g
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/Clone="BOHCQ62"
/clone_lib="BOHC"
/clone_lib="BOHC"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
genomic DNA inserted 219 t
                                                                                           /organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                         Location/Qualifiers
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347 GCAATTAAACATAAGTTTACCTCAGTA 373
                                                                         144 gtcccaccttatattcaagtaggtatgactacaaattttgaaaaatagattgtcacacaat
                                                                                                                227 TCTGAAGCCTTCGGCTAACCGCTATCAGAGAAACCATAGCACCTGACTTTACCTTGTTCA 286
                                                                                                                                                                       167 AGAACATTTTTAAAAACTAAAGAAGATGTAAATTTTCAGTTAAAACCTTTTGTTCACGAC
                                                                                                                                           84
                                                                                                                                                                                       24 aaataacttttgagaaatagaacaaatgaaatcagtttctccaccacttaagtatatctc
              ttagagatctacagcctccctttaggggacatacaaagtcagttgtgttgcctttgttga
                                                        AGACGATCCTTGAATCTTGGAGCTAATTCTTCCCATATCGAACCCCATCTTGCATACAAAA 346
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                            11.9%;
48.8%;
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Pred. No. 36;
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Search completed: September 16, 2002, 01:42:48 Job time: 3301 \sec

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Result
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Copyright (c) 1993 - 2000
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     /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
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/cgn2_6/ptodata/2/ina/6B_COMB.seq: *
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US-09-085-371-5

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US-07-968-971A-10

US-07-968-971A-10

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US-08-889-841B-1
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US-08-889-841B-1
US-08-256-130A-1
US-08-256-130A-2
US-08-816-693A-1
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US-08-215-084A-2
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Million cell updates/sec
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Sequence 1, Appli
Sequence 4, Appli
Sequence 17, Appl
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US-08-998-416-655/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                      TELEPHONE:
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ZIP: 27709
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Sequence 11, Appl	Sequence 11, Appl	Sequence 7, Appli	Sequence 15, Appl	Sequence 15, Appl	Sequence 1, Appli	Sequence 14, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 1, Appli	Sequence 48, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 20, Appl	Sequence 20, Appl

ALIGNMENTS

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US-08-998-416-655/c

Sequence 655, Application US/08998416

Patent No. 6239264

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Pohlmann, Rainer
APPLICANT: Pohlmann, Rainer
APPLICANT: Wendland, Jurgen
TITLE OF INVERTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE NO. 6239264th Carrollina
CITY: Research Triangle Park
STATE: No. 6239264th Carrollina
COUNTRY: USA
ZIP: 27709

COMUTTER EADMABLE FORM:
MEDIUM TYPE: Floppy disk
COMUTTER READMABLE FORM:
MEDIUM TYPE: Floppy disk
COMUTTER READMABLE FORM:
MEDIUM TYPE: Plopsy disk
COMUTTER READMAIL FORM:
MEDIUM TYPE: LANGE 13006/A/CGC1976

TELECOMMUNICATION NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION TON THORMATION:
MEDIUM TYPE: DISC. 1399

INFORMATION FOR SEQ ID NO: 655:

LENGTH: 714 base pairs
TYPE: NO: 629264th Carrollina
COUNTRY: PAGLIA BUP
MOLECULE: PROFILE FORM:
MEDIUM TYPE: Plopsy disk
COMUTTER TONDOMATION

RETEREORY/AGENT NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION DATA:
MEDIUM TYPE: Plopsy disk
COMUTTER THE PROFILE TONDOMATION

RETEREORY/AGENT NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION DATA:
MEDIUM TY
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US-08-998-416-655

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Query Match
Best Local Similarity
""+"hes 17; Conserva
                                                                                    NAME/KEY: CDS
LOCATION: (1)...(1503)
NAME/KEY: misc_feature
LOCATION: (1)...(1503)
OTHER INFORMATION: n = A,T,C or
US-08-889-841B-4
                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-889-841B-4
; Sequence 4, Application US/08889841B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)...(1503)
US-08-889-841B-1
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                                                                                                                                                                                                                                      SOFTWARE: FastSEQ
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08889841B GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                     LENGTH: 1503
TYPE: DNA
ORGANISM: HIV
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES
FILE REFERENCE: 14918-703CIP
                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/676,737 PRIOR FILING DATE: 1996-07-08 NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/889,841B CURRENT FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/676,737 PRIOR FILING DATE: 1996-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE FILE REFERENCE: 14918-703CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: HIV
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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          1.9%; Score 17; DB ilarity 100.0%; Pred. No. 30 Conservative 0; Mismatches
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Pred. No
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            0;
                                        Length 1503;
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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-400-275-17
                                                                US-08-256-130A-1
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US-08-400-275-17
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                             Sequence 1, Application US/08256130A Patent No. 5659121
                                                                                                                                                                                                        Best Local Similarity Matches 17; Conserv
                                                                                                                                                                                                                                       Query Match
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5668295
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wahab, Samir Z.
APPLICANT: Malik, Vedpal S.
TITLE OF INVENTION: PUTRESCHI
TITLE OF INVENTION: RECOMBINI
TITLE OF INVENTION: N. METHYLI
TITLE OF INVENTION: ALTERED NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                     1227 AAATGCAATCAGGAAAG 1243
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY /AGENT INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                      844 aaatgcaatcaggaaag 860
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|||||||||||||||||
| 765 caatttctcaaacaatg 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Creason, Gary L
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER:
FILING DATE: 14-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1251 A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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BIRD, COLIN R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTRESCINE N-METHYLTRANSFERASE, RECOMBINANT DNA MOLECULES ENCODING PUTRESCINE
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Pred. No.
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                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                               Sequence 2, Application US/08256130A Patent No. 5659121
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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APPLICATION UMBER: PCT.GB92.02355

FILING DATE: 18-DEC-1992

ATTONNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.

REGISTRATION NUMBER: 16,773

REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT: HALL, LISA N.
TITLE OF INVENTION: DNA, DNA CONSTRUCT
TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                    APPLICANT: HALL, LISA N.
TITLE OF INVENTION: DNA, DNA CONSTRUCTS, CELLS AND PLANTS
TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                            CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                           NUMBER OF SEQUENCES:
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COMPUTER READABLE FORM:
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                                          CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
               COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                              ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                          BIRD, COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202) 822-0944
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                                                                                                                                                                                              DONALD
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08816693A Patent No. 5874241
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Best Local S
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                              CURRENT AFFILIANT US/08/816, APPLICATION NUMBER: US/08/816, FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5874241thrup, Thoma-
NAME: NO. 5874241thrup, 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                          SOFTWARE: Patentin Relicurrent APPLICATION DATA:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dressler,
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Takahashi, Jos
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrenc
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APPLICATION NUMBER: PCT.
FILING DATE: 18-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Clock Gene and Gene Product NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 tttgtttgttgctctct 726
                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 30-SEP-1994
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                                                                                                                                                                                                                                                           ZIP: 60601
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                                                                                                                                                                                                                                                                                               STATE:
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17; Conservative
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6714627 CUSH
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                                                                                                                            US/08/816,693A
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                                                      Thomas E
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Pred. No.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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; NAME/KEY:
; LOCATION:
US-08-816-693A-1
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; TYPE: DNA
; ORGANISM: Mus musculus
US-08-885-291-1
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US-08-885-291-1/c
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US-09-496-672-1/c
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Matches 17
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Best Local :
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/08/885,291A
CURRENT FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Takahashi, Joseph
APPLICANT: Turek, Fred W.
APPLICANT: Pinto, Lawrence H.
                                                                        CURRENT APPLICATION NUMBER: US/09/496,672
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 08/885,291
PRIOR FILING DATE: 1997-06-30
                                           PRIOR APPLICATION NUMBER: 08/6
PRIOR FILING DATE: 1997-03-13
                                                                                                                                         TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT FILE REFERENCE: 0290-5
SOFTWARE:
SEQ ID NO 1
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                             NUMBER OF SEQ ID NOS:
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Local Similarity 100.0%; Pred. No.
hes 17; Conservative 0; Mismatc
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           PatentIn Ver. 2.0
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Turek, Fred W.
Pinto, Lawrence H.
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                                                             08/816,693
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RESULT 10
US-08-215-084A-2/c
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOOTDEFFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,084
FILING DATE: MARCH 18, 1994
CLASSIFICATION: 435
PRICK APPLICATION DATA:
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APPLICANT: Karen
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FILING DATE: March 24, 1992
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell, Esq.
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: FMC-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215-568-31
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Karen J. Krapcho, Bradford Carr Van APPLICANT: Wagenen, J.R. Hunter Jackson and Robert APPLICANT: M. Kral, Jr. TITLE OF INVENTION: INSECTICIDALLY EFFECTIVE TITLE OF INVENTION: PEPTIDES NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic STRANDEDNESS: TOPOLOGY: lin
115 AATCCAGGGGTCGCCA 100
                                  268 aatccaggggtcgcca 283
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ADDRESSEE: and No. 5461032ris
STREET: One Liberty Place - 46th Floor
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                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
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215-568-3439
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                   1.8%; 5c.
100.0%; Pr
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                                                                                                                                                               Score 16;
pred. No.
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31;
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92;
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RESULT 11 US-08-463-212-2/c

Sequence 2, Application US/08463212 Patent No. 5658563

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RESULT 12
US-08-463-211-2/c
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                                                                                                                                                                                                                                  Sequence 2, Application US/08463211 Patent No. 5658781
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/215,084
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    GENERAL INFORMATION:
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MEDIUM TYPE: 3.5 diskette, COMPUTER: IBM PC compatible
                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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LENGTH: 275 base pairs
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CORRESPONDENCE ADDRESS:
                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                         APPLICANT:
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COUNTRY: U.:
                                                                                                                                                                                                                                                                                                                         115 AATCCAGGGGTCGCCA 100
                                                                                                                                                                                                                                                                                                                                          268 aatccaggggtcgcca 283
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                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: and No. 5658781ris STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: John W. Caldwell, Esq. REGISTRATION NUMBER: 28,937 REFERENCE/DOCKET NUMBER: FMC-0076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: WordPer
                                     STATE:
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16; Conserv
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U.S.A.
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                                                                                                                                                                      M. Kral,
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Jackson, Bradford C. VanWagenen, Rober
                                                                                                                                                                                    Jackson,
                                                                                                                                                                                                     Karen J. Krapcho,
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100.0%; Pr
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Bradford C. VanWagenen, Rober
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Pred. No.
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92;
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US-09-188-930-15
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                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 15
LENGTH: 318
TYPE: DNA
                                                                                                                                                          Query Match
Best Local :
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Best Local Similarity
Matches 16; Conserv
                                                                                                                            Matches
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APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
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ATTORNEY/AGENT I
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LENGTH: 275 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: 08/2
FILING DATE: 18-MAR-1994
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 diskette,
115 AATCCAGGGGTCGCCA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Herewi
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16; Conserv
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                                                                                                                  100.08;
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; Pred. No.
                                                                                                                                                          Score 16;
Pred. No.
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92;
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RESULT 14 US-08-215-084A-6/c ; Sequence 6, Application US/08215084A

Patent No. 5461032

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RESULT 15
US-08-463-212-6/c
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APPLICATION NUMBER: US/08/215,(
FILING DATE: March 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 859,925
FILING DATE: March 24, 1992
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell, Esq.
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: FMC-00
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
TELEFAX: 215-568-319
INFORMATION FOR SED ID NO: 6:
                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08463212 Patent No. 5658563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatc
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Karen J. Krapcho, Bradford Carr Van APPLICANT: Wagenen, J.R. Hunter Jackson and Robert APPLICANT: M. Kral, J. TITLE OF INVENTION: INSECTICIDALLY EFFECTIVE TITLE OF INVENTION: PEPTIDES

NUMBER OF SEQUENCES: 8
                                                                                                                                                                                         TITLE OF INVENTION: INSECTIC TITLE OF INVENTION: PEPTIDES NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        APPLICANT: Karen J. Krapcho, John Randolph Hunter APPLICANT: Jackson, Bradford C. VanWagenen, Robert APPLICANT: M. Kral, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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COUNTRY: U...
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                                                                            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: and No. 5658563ris
STREET: One Liberty Place - 46th Floor
CTY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 429 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                        U.S.A.
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MEDIUM TYPE: 3.5 diskette, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFOCE 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,212
FILING DATE: Herewith
CLASSIFICATION STA
PRIOR APPLICATION NUMBER: 08/215,084
FILING DATE: 18-MAR-1994
APTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell, Esq.
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: FMC-0076
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-463-212-6

Query Match
Best Local Similarity 100.0%; Pred. No. 93;
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0;

Search completed: September 16, 2002, 06:24:30 Job time: 10643 sec

OPRIN MARLE BLANK (USPTO)

1 521 c 2 497 c 3 455 c 4 426 c 5 398 c 6 397 c 7 355 c 9 335 c 10 334 c 11 316 c 12 237 c 13 297 c 14 269 c 16 267 c 17 266	Result No. Score	Pred. No. score gre and is de		Post-processing: Database :	Minimum DB seq Maximum DB seq	Total number of	Word size :	Q.	Title: Perfect score: Sequence: Scoring table:	Run on:	OM nucleic - n	
58.2 . 613 10 55.5 498 10 50.8 426 9 47.6 426 9 44.5 504 9 44.4 5397 9 39.7 477 9 39.7 563 9 37.3 820 10 37.3 429 9 33.2 297 9 33.2 297 9 34.2 297 9 35.3 491 9 36.3 491 9 37.3 491 9 37.3 491 9 38.2 297 9 39.4 491 9 29.8 270 9 29.8 270 9 29.8 261 9	% Query Query Match Length DB ID	is the number of ater than or equal rived by analysis		Listing first 45 EST:*	length: 0 length: 2000000000	f hits satisfying chos	0	Gapop 60.0 , Gapext 13736207 seqs, 6748	US-09-700-770-5 895 1 ctaatctgttacgtaacagc	September 16, 2002,	nucleic search, using	GenCore Copyright (c) 1993
BC536626 BF196945 AI340056 AA4479746 AA481852 AI142875 BE148882 AI079445 BI770944 AA430487 AW298444 AA317141 AI830551 AI860310 AW770737	SUMMARIES	results predicted by chance to 1 to the score of the result bei of the total score distribution		summaries		en parameters:		pext 60.0 6748477542 residues	:	05:18:16 ; Search (without 4002.934	sw model	re version 4.5 93 - 2000 Compugen Ltd.
BG536626 602566231 BF196945 7180f03.x A1340056 gn18h09.x AA479746 zu35g03.s A1809681 wf76c06.x AA481852 zv42f04.r A1142875 zv542f04.r A1172876 zv54606.s BE148882 CM2-HT024 A1079465 oz39f05.s BI770944 603059769 AA430487 zw23f06.s AW298444 UI-H-BW0-AA317141 EST19048 A1830551 wf51b02.x A1860310 wf01e10.x A1276107 g174h09.x AW770737 h189g02.x	Description	e to have a t being printed, ution.				27472414			aataaatatttttaaatgtc 895	time 3017.73 Seconds alignments) Million cell updates/sec		
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL RESULT 1
BG536626
LOCUS
DEFINITION PATURES OMMENT source found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLCM1509 row: m column: 07
High quality sequence stop: 611.
Location/Qualifiers BG536626 613 bp mRNA linear EST 03-APR-2001 602566231F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691118 5', mRNA sequence. BG536626 BG536626.1 /organism="Homo sapiens"
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/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note= GI:13528159 .613

BASE CO

COUNT

165

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kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto. CA). Note: this is a NIH_MGC Library."

a 176 c 132 g 140 t

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REFERENCE
AUTHORS
TITLE
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BF196945/c
LOCUS
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ORGANISM
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                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 498)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro-
                                                                                                                                                                                             BF196945 498 bp mRNA
7180f03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 I
IMAGE:3527932 3', mRNA sequence.
  This
                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                              human.
                                                                                                                                                                        BF196945.1
                                                                                                                                                                                      BF196945
  clone
 cgapbs-r@mail.nih.gov
lone is available roya
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through
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Вр

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QΥ

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Query Match
Best Local Sim
Matches 571;

Similarity

58.2%; 99.8%;

Conservative

0;

Score 521; DB 10; Pred. No. 1.3e-260; 0; Mismatches 1;

Length

613;

Indels

0;

0

Db

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T. asea

RESULT 3 AI340056/c

LOCUS

AI340056

491 ďď

mRNA

linear

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13-FEB-1999

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BASE CO
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Matches 49
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Best Local
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18
                                                                acaccaaaggcaccacagaaagccaaaccaagcattccagagcctgccagcaatttctcaa 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgggctgccaaagaagcagtgcccctgtgatcatttcaagggcaatgtgaagaaaacaag 458
                              aaatatttttaaatgtc
                                                                                                                                                                                                                                                                     GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGC
                                                                                                                                                     gtgccctccccttacccaggcttaggcttaattacctgaaagattccaggaaactgtagc
                                                                                                                                                                                                   TTCAAGATCATTTTGTTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
                                                                                                                                                                                                                       ttcaagatcattttgtttgttgctctctctagtgtcttcttcttctctcgtcagtcttagcct
                                                                                                                                                                                                                                                                                                                                                                                                         ACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                         acaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
497; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov)
High quality sequence stop: 487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.5%;
nilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Forgan: pooled; vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSP pool 1: 150407, 151176-152327 Soares NbHSP pool 1: 150407, 151176-152327 Soares NbHSP pool 1: 758280-760583, 772104-774407 Soares NbHSP pool 1: 758280-756407, 739080-74099 Subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3527932"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 497; DB 10; pred. No. 4.3e-248; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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ORGANISM
                      δÃ
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ORIGIN
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Best Local Similarity
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                          519
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                                                                                                                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                                                                                                                       acaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttcc
                                                                                                                                                           tgggctgccaaagaagcagtgcccctgtgatcatttcaagggcaatgtgaagaaacaag
                                                                                                                                                                                                                                        agaatgtgagtgcaaagattggttcctgagagccccgagaagaaaattcatgacagtgtc
                                                                             acaccaaaggcaccacagaagccaaacaagcattccagagcctgccagcaatttctcaa
                                                                                                                                                                                                                    AGAATGTGAGTGCAAAGATTGGTTCCTGAGAGCCCCCGAGAAGAAAATTCATGACAGTGTC
                                                                                                                                                                                                                                                                                             CGCCAGAGGCCACAGGCCAGGCCTTCTAGGAGATGGCTCCAGGAAGGCGGCCA
                                                                                                                                                                                                                                                                                                                cgccagaggccacagggaccgaggccaggcttctaggagatggctccagggaaggcggcca
                                                                                                                                      TGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAG
                                                         ACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
AI340056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 485 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 485 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI340056.1 GI:4076983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1898657"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Lu5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 455; DB 9; L
Pred. No. 3.6e-226;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 491;
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529 426 469

ctaagaagctttgctctgcctttgtaggagctctgagcgcccactcttccaattaaacat 588 CACCACAGAAAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAG caccacagaaagccaaacaagcattccagagcctgccagcaatttctcaaacaatgtcag Matches

426;

Conservative

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BASE COUNT
ORIGIN
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                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 bp mRNA linear EST 08-1
zu35g03.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:740020 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moo Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                121
                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:740020"
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:5939727"
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /clone_lib="Soares ovary tumor NbHOT"
                47.6%;
                                                                                                64 c
Score 426; DB; Pred. No. 4.7 0; Mismatches
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                DB 9; Lo
4.7e-211;
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                                Length 426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore, B.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI809681 504 bp n
wf76c06.xl Soares_NFL_T_GBC_S1 Homo
IMAGE:2361514 3', mRNA sequence.
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy
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            134
                                                                    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
        from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by E Soares and M. Fatina Bonaldo. "
                                                                                                                                                                                      /clone="IMAGE:2361514"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Unpublished (1997)
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IMAGE:756319 5', mRNA sequence.
AA481852
                                                                                                                                  This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further Seq primer: -2@ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                           Washington University School of Medicine Washington University School of Medicine
                                                                                                                                                                                                          Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                  Contact: Wilson RK
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                                                                                                                                                                                          est@watson.wustl.edu
              /clone_lib="Soares
/sex="Female"
                                                /db_xref="taxon:9606"
/clone="IMAGE:756319"
/tissue_type="ovarian tumor"
                                                                                   /organism="Homo sapiens"
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     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anat
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Pred. No. 6.4e-1
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IMAGE:1661122
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Matches 475; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                                                                                                                          CM2-HT0244-221199-038-f02
BE148882
                                                                    Homo sapiens
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/db_xref="taxon:9606"
/clone="IMAGE:1661122"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnant uterus
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oz39f05.s1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the
Project. This entry can be seen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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199-038-f02&t3=1999-11-22&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0244"
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IMAGE:1677729
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                                                                    AAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCATTTAACCTTAAATGCAATCAGG
                                                                                                                                                             cttctctcgtcagtcttagcctgtgccctccccttacccaggcttaggcttaattacctg 796
                                                                                                                                                                                                                                                                                      AGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACC
AAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 921 Std Error: 0.00
Seq primer: -40ml3 fwd. Erf from Amersham
High quality sequence stop: 431.
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AI079465.1 GI:34
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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pregnant uterus"
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/clone_lib="Soares_NhHMPu_S1"
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Pred. No. 1.2e-165;
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678 gtgctctcaaaaagcatgtttttcaagatcattt 711
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                                                                                                                                                                                                                                                                                                                                                                270 AAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATTTCAA 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 820)
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603059769F1 NIH_MGC_122
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Plate: LLAM11524 row: j column: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/db_xref="taxon:9606"
/clone="IMAGE:5209073"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
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TTTGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTATTCCAATTAAACATTCTCAGCCA
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Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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WashU-Merck EST Project 1997
Unpublished (1997)
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zw23f06.sl Soares ovary tumor IMAGE:770147 3', mRNA sequence
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Fax: 314 286 1810
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1 (bases 1 to 419)
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/db_xref="GDB:5980022"
/db_xref="taxon:9606"
/clone="IMAGE:770147"
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M.Fatima Bonaldo. "
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99.5<del>8</del>;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortlum/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW298444 429 bp mRNA linear EST 16-JAN-: UI-H-BW0-ajl-e-06-0-UI.sl NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732243 3', mRNA sequence.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/clone_lib="NCI_CGAP_Sub6"
//clone_lib="NCI_CGAP_Sub6"
//ab_host="DH10B (Life Technologies)"
//ab_host="DH10
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/db_xref="taxon:9606"
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Primates;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 ttgctc 723
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           C.J., Lee, N.H., Kirkness, E.F., Weinstcok, K.G., Gocayne, J.D., White (O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald (L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, T.A., Collins, E.J., Lingham, C., Colleman, T.A., Collins, E.J., Condition, Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman, Collins, E.J., Colleman,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA317141 297 bp
EST19048 Lung Homo sapiens cDNA
AA317141
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 297) Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
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Subtraction was performed as previously described [Bonaldo , Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_LIB-NCI_CGAP_LU13
TAG_TISSUE=lung
TAG_SEQ-eCCGG"
112 g 140 t 3 others
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99.7%;
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pred. No. 4.1e-153;
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5' end, mRNA sequence.
Fischer, C.,
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     Hastings, G.A.,
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        He, W.W
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Feng, D.-F.,

Ferrie, A.,

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RESULT 14
AI830551/c
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KEYWORDS
                   REFERENCE
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                                                                                                                                                                                                                                                                                               Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                             mRNA sequence.
AI830551
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wj51b02.x1 NCI_CGAP_Lu19
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
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Contact: Kerlavage,
               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 491)
                                                                                                             AI830551.1
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                                                                      Homo sapiens
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                           human.
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/note="Organ: lung; Vector:
; Site_2: XhoI"
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/db_xref="taxon:9606"
/clone_lib="Lung"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
AI860310.1
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                           mRNA sequence.
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/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2406315"
/clone_lib="NCI_CGAP_Lul9"
/tissue_type="squamous cell carcinoma,
/tissue_type="squamous cell carcinoma,
differentiated (4 pooled tumors, includ
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40Up from Glbco
High quality sequence stop: 262.
Location/Qualifiers
1 270.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage-resistant)"
/note="Organ: lung: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2423658"
/clone_lib="NGI_GGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AE148882
AA430487
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B1770944 603059769
BG536626 602566331
AW471176 xx13a03 x
BF196945 7180f03 x
A1340056 qn18h09 x
A1809581 wf76c06 x
A1830551 wj51b02 x
BF061539 7j52910 x
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A1276107 q174h09 x
BE144882 CW2-HT024
AA479746 zu35g03 x
AA430487 zw33f06 s
AW298444 UT-H-BW0-
A1079465 oz39f05 x
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4.4 4.5	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18
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BF743524 QV0-BT084 AW389442 IL0-ST016	AA477092 zu35g03.r	BG535485 602563170	BI078998 602873258	BE181362 CMO-HT063	BE197231 ug73b06.y	AI207071 qf80f02.x	AA789593 vw61f07.r	AA881969 vx31g04.r	AA537274 vk46b02.r	BE624584 uu23h11.y	BF055365 7j78f09.x	BE645174 7e64d07.x	AI368232 qwl6e02.x	AI860310 wl01e10.x	AA366288 EST77218	BM430624 1Duo02C09	AW183010 xp99f12.x	AW770575 hl86g07.x	AA317141 EST19048	BF882906 QV3-ET020	BF743581 QV0-BT084	AW173795 xp98g10.x	BF745586 QV0-BT084	BE073132 MR3-BT055	AW770737 hl89g02.x	AA433968 zw23f07.r

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ALIGNMENTS

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	FEATURES Source		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BI770944 LOCUS DEFINITION
/Organism="Homo saplens" /Organism="Homo saplens" /Olone="TwaGE:5209073" /Clone=!ib="NuAGE:5209073" /Clone=!ib="NuH_MGC_122" /Lab_host="DH10B" /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size	High quality sequence stop: 772. Location/Qualifiers 1. 820	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11524 row: j column: 18	1 (bases 1 to 820) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) . Contact: Robert Strausberg, Ph.D.	B1770944.1 GI:15762522 B1770944.1 GI:15762522 EST. Human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	BI770944 820 bp mRNA linear EST 25-SEP-2001 603059769F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209073 5', mRNA sequence.

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a 237 c 162 g 196 t
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High quality sequence stop: 611.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distr
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone_lib="NIH_MGC_77"
/lab_msot="DH10B (TI phage-resistant)"
/lab_msot="Ph10B (TI phage-resistant)"
/lab_msot="
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/db_xref="taxon:9606"
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Pred. No. 4.2e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
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xv13a03.x1 Soares_NFL_T_GBC_S1 Homo
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2812972"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.8e-121;
"" matches 58;
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/db_xref="taxon:9606"
                                                                                            /clone="IMAGE:3527932"
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                                                                                                                                                                                                                             Tumor Gene Index (1997) (1997) (1997) (20 contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Email: cgapbs-r@mail.nih.gov free through LLNL IMAGE Consortium (info@image.llnl.gov) for further High quality sequence stop: 487.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 498)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was
                                                                                                                 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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              Tumor Gene Index
Unpublished (1997)
                                      NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Traffitute, Cancer Genome Anatomy
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 491)
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Robert Strausberg,
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IMAGE:1898657 3',
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.I.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sec

Clone distribution: NCI-CGAP clone distribution in:

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 485 Std Error: 0.00
                                                             cgccagaggccacagggaccgaggccaggcttctaggagatggctccaggaaggcggcca 338
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                 ttcaagatca 708
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: lung; Vector: pT/TJD-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/TJ3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 488.4;
Pred. No. 9.6
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AUTHORS
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AI809681/c
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                                                                                                                                   CTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTC
                                                                   TTCTCCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAG
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1 (bases 1 to 504)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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AI809681.1 GI:5396247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE Consortium (info@image.llnl.gov) for Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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Query Match
Best Local Similarity
Matches 477; Conser

52.6%; nilarity 97.1%; Conservative

Score 471; DB Pred. No. 3.1e 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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Seq primer: -40UP from Gibco
High quality sequence stop: 463.
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                                                                                   Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and Patima Bonaldo. "
                                       Fatima Bonaldo. '
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differentiated (4 pooled tumors, including pr
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/clone="IMAGE:2406315"
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                                       4 others
                                                                                                           by Bento Soares and M.
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                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 482)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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482 bp mRNA linear 7j52g10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens IMAGE:3390114 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Location/Qualifiers
/note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from
                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3390114"
/clone_Lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/clo_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                     GI:10820370
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                                                                                                                                                                                                                  ox64e06.sl Soares_NhHMPu_Sl Homo
3', mRNA sequence.
AII42875
AII42875.1 GI:3659234
EST.
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.go
                                                                                                                    Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 477)
                                        Unpublished (1997)
                                                           Tumor Gene Index
                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
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99.2%;
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Pred. No. 9.7e-110;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                477 bp
                    Ph.D
                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              mRNA linear EST 23-OCT-1998 sapiens cDNA clone IMAGE:1661122
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                                                                                                                                                               AAGACAGTGAGCACCTACCAGACACTCTTCTTCTCCCACCTCACTCTCCCACTGTACC
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A1276107 461 bp
q174h09.x1 Soares_NhHMPu_S1 Homo
3', mRNA sequence.
A1276107
A1276107.1 G1:3898381
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h quality sequence stop: 383.
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/tissue_type="Pooled human me
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                                      sapiens cDNA clone
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                                                 linear
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aagggcaatgtgaagaaaacaagacaccaaaggcaccacagaaagccaaacaagcattcc 495
                                                                      gaaagattccaggaaactgtagcttcctagctagtgtcatttaaccttaaatgcaatcag 855
                                                                                                                                                                    tcttctctcgtcagtcttagcctgtgccctccccttacccaggcttaagcttaattacct
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gaaagtagcaaacagaagtcaataaatatttttaaatgtc 895
                                                                                                                                                                                                                                      GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACA-
                                                                                                                                               TCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 412 Std Error: 0.00 Seq primer: -40UP from Gibco.
Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, | Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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22 a 74 c 128 g 136 t 1 others
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/tissue_type="Pooled human melanocyte,
pregnant uterus"
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/db_xref="taxon:9606"
/clone="IMAGE:1878113"
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98.9%;
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Pred. No. 4.3e-101;
0; Mismatches 3;
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     141
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                                                                                                                                                                                                                Local Similarity
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CACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCT 200
                                                              ATCTCTCAAACAATGTCAGCTAAGAAGCTTCGCTCTGCCTTTGTAGGAGCTCTGAGCGCC
                                                                             atttotcaaacaatgtcagctaagaagctttgctctgcctttgtaggagctctgagcgcc 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM2-HT0244-221
199-038-f02&t3=1999-11-22&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: puc 18 forward
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CM2-HT0244-221199-038-f02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence start: 26 quality sequence stop: 562.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 D
                                                                                                                                                                                                                                                                                       /note="organ: head_neck; vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORSSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone_lib="HT0244"
                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism≃"Homo sapiens"
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                                                                                                                                                                                                              47.8%;
98.9%;
                                                                                                                                                                                                             Score 427.6; DB 9;
Pred. No. 5.4e-100;
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HT0244 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estéwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel, Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Mart, Schellenberg,K., Steptoe,M., Tan,F., Theising,B., T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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zu35g03.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:740020 3', mRNA sequence.
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EST.
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Location/Qualifiers
                                                 (Pharmacia). Library
M.Fatima Bonaldo. "
a 64 c 122 g
                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:5939727"
/db_xref="taxon:9606"
/clone="IMAGE:740020"
                                                                                                                                                                                                                                                       /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  School of Medicine way, Box 8501, St. 1
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RESULT 13
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                                                                                                                                                                 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                zw23f06.s1 Soares ovar
IMAGE:770147 3', mRNA
                                 This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further: Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 356.
                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1810

Fax: 314 286 1810
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AA430487.1 GI:2111061
EST.
                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                       (bases 1 to 419)
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/organism="Homo sapiens"
/db_xref="GDB:5980022"
                                                                                                                                                                                                                                                    Eutheria;
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Primates;
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RESULT 14
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AW298444
AW298444.1
EST.
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UI-H-BW0-ajl-e-06-0-UI.sl NCI_CGAP_
                                                                                                 IMAGE: 2732243
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/lab_host="DH10B (ampicillin resistant)"
/note="organ: ovary; Vector: pT7T3D (Pharmacia) with modified polylinker; Site_1: Not I; Site_2: Eco RI; J strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) prime strand cDNA was primed with a Not I - oligo(dT) primed wi
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/sex="Female"
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                                                                                             3', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 414.8; DB 9;
Pred. No. 1.1e-96;
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mo sapiens
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CDNA clone
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Unpublished (1237)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A strand cDNA and therefore this may represent a bonafide poly A

Tumor Gene Index Unpublished (1997)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 429) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Pro

Project

Euteleostomi;

Homo sapiens

GI:6705080

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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 409; Conserv
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9taggagctctgagcgcccactcttccaattaaacattctcagccaagaagacagtgagc 611
                                                                                                                   TTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTT
                                                                                                                                                      ttccagagcctgccagcaatttctcaaacaatgtcagctaagaagctttgctctgccttt 551
                                                                                                                                                                                                                                          TTTCAAGGGCAATGTGAAGAAAACAAGACAACCAAAGGCACCACAGAAAGCCAAACAAGCA
                                                                                                                                                                                                                                                                         tttcaagggcaatgtgaagaaacaagacaccaaaggcaccacagaaagccaaacaagca 491
                                                                                                                                                                                                                                                                                                                                                                 CCCGAGAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       taggagatggctccaggaaggcggccaagaatgtgagtgcaaagattggttcctgagagc 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="InagE:733243"
/clone_lib="NCI_CGAP_Sub6"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="Wector: pT773D-Pac (Pharmacia) with a modified
/note="Wector: pT773D-Pac (Pharmacia) with a modified
/note="Wector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BW, which consists of
a mixture of four normalized libraries: NCI_CGAP_Sub6
library had 7 million recombinants. A single-stranded DNA
preparation of BW was used as a tracer in a subtractive
hybridization with a driver comprising: the IMAGE pool
(NCI_CGAP_Kid3 pool 1 LLAM 334-337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911,
1456008-1456775,1500552-1502855); NCI_CGAP_Kid5 pool 1
LLAM 3338-3342,3722-3725, 3776-3778 (IMAGE CloneIDs
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE
CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4
pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631,1469064-1470983, 1475592-1476743);
NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-110199,
1217928-1220615); NCI_CGAP_Col0 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255,1144584-1145351).
(50% of the driver population), plus a pool of 3,840
arrayed clones from NCI_CGAP_Sub1 (IMAGE CloneIDs
2708616-2712455) and NCI_CGAP_Sub1 (IMAGE CloneIDs
2710456-2723591) (30% of the driver population), plus a
pool of fill36 clones from NCI_CGAP_Sub3 (IMAGE CloneIDs
2712456-2723591) (30% of the driver population).
Subtraction was performed as previously described (Bonaldo
Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Two Approaches To Facilitate Gene Discovery. Genome
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Pred. No. 3.4e-95;
0; Mismatches 3
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SOURCE
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AI079465/c
                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                gctaagaagctttgctctgcctttgtagg-agctctgagcgcccactcttccaattaaac 586
                                                                                                                                                       GCACCACAGAAAGCAAACAAGCATTCCAGAG-CTGCCAGCAATTTCTCAAACAATGTCA 373
ATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCCACCTCACT
                                                                          GCTAAGAAGCTTTGCTCTGCCTTTGTAGGCAGCTCTGAGCGCCCACTCTTCCAATTAAAC
                                                                                                                                                                                                                                          427;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 921 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1079465 431 bp oz39f05.1 Soares_NhHMPu_S1 Homo 3', mRNA sequence.
                                                                                                                                                                                                                                                        h 45.3%;
Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI079465.1 GI:3415716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pregnant uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1677729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_NhHMPu_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         host="DH10B"
                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                 Score 405; DB 9; 1
Pred. No. 3.7e-94;
0; Mismatches 0;
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IMAGE:1677729
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Search completed: September 16, 2002, 01:42:54 Job time: $3307 \ \text{sec}$

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   length: 0
length: 2000000000
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| Cgn2_6/ptodata/2/ina/5A_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| Cgn2_6/ptodata/2/ina/backfiles1.seq:*
| Cgn2_6/ptodata/2/ina/backfiles1.seq:*
| Cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-232-463-14
US-09-007-005-17
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US-09-244-796-17
US-09-244-796-17
US-09-248-986-3
US-08-931-999-4
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US-08-931-999-4
US-08-931-999-3
US-08-791-26-62
US-08-791-3-83-5
PCT-US94-05365-5
PCT-US94-05365-5
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PCT-US94-05365-5
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PCT-US94-05365-5
PCT-US94-05361-3
US-08-791-0340-1
US-08-971-036-1
US-09-096-577-01
US-09-096-577-17
US-09-252-816A-7
US-08-836-567-11
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53, Appl
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15, Appl
16, Appl
174, Appl
175, Appl
176, Appl
176, Appl
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US-08-232-463-14
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Sequence 14, Application US/08232463 Patent No. 5670367
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                  TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)863-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
     IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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FILING DATE:
APPLICATION NUMBER: EP 91 114 300
FILING DATE: 26-AUG-1991
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CITY: Alexandria
STATE: VA
                                                                                                         STRANDEDNESS:
TOPOLOGY: 11r
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ZIP: 22313-0299
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pTZgpt-F1s
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1800 Diagonal Road,
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                                                      INFORMATION FOR SEQ ID NO:
                                                                                              FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-3300
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
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                                                                                   TELEFAX:
 STRANDEDNESS:
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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CITY: Alexandria
                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                         7218 base pairs
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                                                                                   (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foley & Lardner
                                                                                                                                                                                        UMBER: EP 91 114 300.6
26-AUG-1991
single
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8.8%; Pred. No. 3.9e-08;
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; FEATURE:

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; OTHER INFORMATION: n = A,T,C

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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
                                                                                                                       Matches
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09007005B Patent No. 6258558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Riche
TITLE OF INVENTION: SELECTION OF PROTEINS
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: line
IMMEDIATE SOURCE:
CLONE: pTZgpt-
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                                                                         624 cactettetteteceaceteacteteceactgtacceacectaaateattecagtgete 683
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                                                                                                                       Conservative
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                                                                                                                                       5.3%;
                                                                                                                                                         3.8%;
                                                                                                                     91;
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Pred. No. 0.2;
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                                                                                                                     Mismatches
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                                                                                                                                                         DB 4;
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                                                                                                                                                       Length 289;
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RESULT 5
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                                   Sequence 53, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/07,005
EARLIER FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
   APPLICANT:
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
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 Duclert, Aymeric
                 Dumas Milne Edwards,
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Pred. No. 0.2;
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                   Jean-Baptiste
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US-09-228-986-3
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                                                                                                                                                                                    Sequence 3, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
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SEQ ID NO 53
SEQ ID NO
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Best Local
                                                   TITLE OF INVENTION: Compositions Isolated from Plant Cells TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling FILE REFERENCE: 11000/1020 CURRENT APPLICATION NUMBER: US/09/228,986 CURRENT FILING DATE: 1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                               APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Niels
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EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/091,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
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                                 NUMBER OF SEQ ID NOS:
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                 SOFTWARE: FastSEQ for Windows Version
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LOCATION: 81..152
OTHER INFORMATION: Von Heijne matrix
OTHER STREAMTON: SCORE 6.2
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70; Conservative
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429..445
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406..411
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Length 445; Indels

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326 274 266

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LENGTH: 2686

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US-08-458-568A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08458568A Patent No. 5821339
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Best Local Similarity 45.9%;
Matches 112; Conservative
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                                                  TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/065,146
FILING DATE: 05-MAY-1993
                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No.
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schaffer, Priscilla APPLICANT: Yeh, Lily TITLE OF INVENTION: Composition TITLE OF INVENTION: Infections
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
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                                                                                                                                           REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI-0029
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995
 STRANDEDNESS:
                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                 LENGTH:
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SYSTEM: PC-DOS/MS-DOS
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double
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Pred. No. 1.5;
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Best Local :
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Iandolo, JAPPLICANT: Crupper, STITLE OF INVENTION: BUUMBER OF SEQUENCES:
   ORIGINAL SOURCE: ORGANISM: Sta
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                HYPOTHETICAL:
ANTI-SENSE: 1
                                                           TOPOLOGY: un
MOLECULE TYPE:
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ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type
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HYPOTHETICAL: N
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                                                                                                                                                                                                                NAME: Collins, John M. REGISTRATION NUMBER: 26 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        731 tgtc 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Boulevard, Suite 400 CITY: Kansas City
                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                           nucleic acid
EDNESS: double
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Staphylococcus aureus
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Broad Spectrum Chemotherapeutic Peptide
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54.0%;
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Pred. No. 3.
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Best Local Similarity 75.5
Conservative
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Patent No. 6031075
                                                                      Query Match
Best Local :
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TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fast-SEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-241-2324
                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Josephic, David J
REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
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              214 tccctcctcctgttgccactaatgctgatgtccatggtctctagcagcctgaatcca 273
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CITY: CINCINNATI
                                                                                                                                                                                  NAME/KEY: Coding Sequence LOCATION: 1...1143
OTHER INFORMATION:
                                                                   Local
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                                                                                                                                                      NAME/KEY: Signal Sequence LOCATION: 1...601
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10 TCACACCTGCTGCAGTGGCTGCTGCTGCTGCCCACGCTCTGTGGCCCAGGCACTGCT 69
                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                     Similarity
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05-FEB-1996
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MATURE ALVEOLAR SP-B AND A
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75.5%;
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                                                     Score 31.6; DB Pred. No. 2.3; 0; Mismatches
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Pred. No. 4;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-126-109-9
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 Matches
                Best Local
                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: McMillian, Nabeela
                                                                                                                                                                                                                                                                                                FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UI
FILING DATE: 03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                        REGISTRATION NUMBER: P-4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                          : (512) 418-3000
(512) 474-7577
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Hugl, Sigrun R.
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Newgard, Christopher
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                                                                                       DNA (genomic)
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               3.5%;
58.7%;
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             Score 31.2;
Pred. No. 4
 Mismatches
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                .6;
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                             4.
 38;
                             Length 2264;
   0;
Gaps
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379 agaaaattcatgacagtgtctgggctgccaaagaagcagtgcccctgtgatcatttcaag 438

270 AGAGAATTCCTGAGAGAGTTGTGCATGCTAAAGGAGCAGGGGCCTTTGGCTACTTTGAGG 329

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RESULT 12
US-08-073-383-5/c
: Sequence 5, Application US/08073383
; Patent No. 5443962
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Best Local Similarity
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Patent No. 5821091
GENERAL INFORMATION:
                                                                          GENERAL INFORMATION:
                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/592,126 FILING DATE:
                                                                                                                                                                               1318 CCATCTTCCCTGTGGTCCCACGACTGCTGAACCGGATGTACGACAGGATCTTCA 1265
                                                                                                                                                                                                                                         1378 TTGGCTTCTTCCAGGGAGATATCCGCCTTCTCTCAGATGACATGAAGGCTCTATGCCCCA 1319
            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
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ANTI-SENSE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                   215
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Cottarel, Guillaume
Damagnez, Veronique
VENTION: [fillin "Insert Title of Application"|ASSAY AND REAGENTS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                        Draetta, Giulio
                                                                                                                                                                                                                                                                                                          Conservative
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Polypeptides
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RESULT 13
US-08-328-239A-3/c
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                                                                                                                                                                                                                       Sequence 3, Application US/08328239A Patent No. 6037136 GENERAL INFORMATION:
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Best Local :
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TELEFAX: (617) 227-59
INFORMATION FOR SEQ ID NO:
                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HO
                                                                                                                                           APPLICANT: Jessus, Catherine
TITLE OF INVENTION: Interactions between Raf Proto-Oncogenes
TITLE OF INVENTION: and CDC25 Phosphatases, and Uses Related
                                                                                                                                                                           APPLICANT: Beach, David H.
APPLICANT: Galationov, Konstantin
APPLICANT: Jessus, Catherine
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REGISTRATION NUMBER: 36,705
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
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LENGTH: 2062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UPTILING DATE: 19930604 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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STREET: ...
STREET: MA
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LOCATION:
                ZIP:
                                                             ADDRESSEE: FULL, ADDRESSEE: One Post Office
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nes 53; Conserv
                                 COUNTRY:
                                                STATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                           and CDC25 Phosphatases, and Uses Related Thereto
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Pred. No. 5
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Gaps

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MEDIUM TYPE:

Floppy disk

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

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US-08-328-239A-3
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PCT-US94-06365-5
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                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 04-JUN-1993
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2062 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUS9406365 GENERAL INFORMATION:
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Best Local :
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LENGTH: 2062 base pairs
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
ABBIICATION NUMBER. DOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 832-7000
TELEFAX: (617) 832-7000
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                           FEATURE:
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                                                         MOLECULE TYPE:
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OPERATING SYSTEM: PC-I
OPERATE: ASCII(Text)
OPERATE: ASCII (Text)
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nes 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CS
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                                                                         STRANDEDNESS:
TOPOLOGY: li
                            NAME/KEY:
                                                                                                  TYPE: nucleic acid
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            CDS
211..1631
                                                                       linear
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06-JUN-1994
                                                                                      single
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Pred. No. 5
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Best Local Similarity
Thes 53; Conserve
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PCT-US95-13661-3/c
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PCT-US95-13661-3
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                                                                                                               Matches
                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII(Text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
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APPLICANT: Galatic
APPLICANT: Jessus
                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                          TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Galationov, Konstantin APPLICANT: Jessus, Catherine TITLE OF INVENTION: Interactions | TITLE OF INVENTION: and CDC25 Pho:
 902
               733 tcttcttctctcgtcagtcttagcctgtgc 762
                                                                      733 tcttcttctctcgtcagtcttagcctgtgc 762
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                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                NAME/KEY:
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TTTTCCACCTGCTTCAGTCTTGGCCTGTTC 873
                                                      TTTCCTTGGCCAGAAAAATACTTTTTTTAACTTTATCTGGTATTGTGTTGTCCTTGAAT 903
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                                                                                                                            Similarity
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58.9%;
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                                                                                                             Score 30.8; DB Pred. No. 5.8; 0; Mismatches
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Pred. No. 5.8;
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Search completed: September 16, 2002, 03:27:01 Job time: 9344 sec